

GenCore version 5.1.6
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OM nucleic - nucleic search, using BW model

Run on: September 9, 2005, 10:16:59 ; Search time 1710 Seconds
(without alignments)
1118.223 Million cell updates/sec

Title: US-09-981-151D-7
Perfect score: 2895
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7351250 seqs, 3283620254 residues

Total number of hits satisfying chosen parameters: 14702500

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2675.4	92.4	2997	10	US-09-981-151A-1 Sequence 1, Appli
3	1877.8	64.9	3675	17	US-10-330-176-1 Sequence 1, Appli
4	1877.8	64.9	3675	18	US-10-275-107-16 Sequence 16, Appli
5	1874.6	64.8	3675	13	US-10-217-774-3 Sequence 3, Appli
6	1874.6	64.8	3675	15	US-10-296-616-1 Sequence 1, Appli
7	1874.6	64.8	3675	21	US-10-804-457-3 Sequence 3, Appli

8	1874.6	64.8	4042	13	US-10-217-774-5	Sequence 5, Appli
9	1874.6	64.8	4042	21	US-10-804-457-5	Sequence 5, Appli
10	1795.6	62.0	2433	10	US-09-981-151A-3	Sequence 3, Appli
11	1695	58.5	2902	10	US-09-981-151A-5	Sequence 5, Appli
12	1638	56.6	4888	17	US-10-399-645-19	Sequence 19, Appli
13	709.6	24.5	3389	18	US-10-363-937-34	Sequence 34, Appli
14	708	24.5	3219	18	US-10-354-983-3	Sequence 3, Appli
15	708	24.5	3663	18	US-10-354-983-1	Sequence 1, Appli
16	708	24.5	3666	16	US-10-240-545A-1	Sequence 1, Appli
17	706.4	24.4	2805	18	US-10-275-107-18	Sequence 18, Appli
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32	433.8	15.0	1986	18	US-10-354-983-7	Sequence 7, Appli
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40	241.2	8.3	2217	14	US-10-226-560-6	Sequence 6, Appli
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42	233.8	8.1	624	17	US-10-188-186-155	Sequence 155, App
43	227	7.8	2274	9	US-09-963-791-23	Sequence 23, Appli
44	227	7.8	2274	17	US-10-419-276-23	Sequence 23, Appli
45	227	7.8	2274	24	US-11-027-743-23	Sequence 23, Appli

ALIGNMENTS

RESULT 1
US-09-981-151A-7
Sequence 7, Application US/09981151A
Publication No. US20030212256A1
GENERAL INFORMATION:
APPLICANT: Edinger, Shlomit R
APPLICANT: Gerlach, Valerie
APPLICANT: MacDougall, John R
APPLICANT: Malyankar, Muriel M
APPLICANT: Smithson, Glenda
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A
APPLICANT: Stone, David J
APPLICANT: Gunther, Erik
APPLICANT: Ellerman, Karen
APPLICANT: Shimkets, Richard A
APPLICANT: Padigaru, Muralidhara
APPLICANT: Guo, Xiaojia
APPLICANT: Patturajan, Meera
APPLICANT: Taupier Jr, Raymond J
APPLICANT: Burgess, Catherine R
APPLICANT: Zerhusen, Bryan D
APPLICANT: Kekuda, Ramesh
APPLICANT: Spytek, Kimberly A
APPLICANT: Gangolli, Esba A
APPLICANT: Fernandes, Elma R
APPLICANT: Gorman, Linda
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-168
CURRENT APPLICATION NUMBER: US/09/981, 151A

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; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 60/241,040
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,058
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; PRIOR APPLICATION NUMBER: 60/241,063
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,243
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/242,152
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/242,482
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,611
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,612
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,880
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/242,881
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 2895
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-981-151A-7

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; Publication No. US20030212256A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Gerlach, Valerie
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Muriel M
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A
; APPLICANT: Stone, David J
; APPLICANT: Gunther, Erik
; APPLICANT: Ellerman, Karen
; APPLICANT: Shimkets, Richard A
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Guo, Xiaojia
; APPLICANT: Patturajan, Meera
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Burgess, Catherine E
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Gangolli, Esha A
; APPLICANT: Fernandes, Elma R
; APPLICANT: Gorman, Linda
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-168
; CURRENT APPLICATION NUMBER: US/09/981,151A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 60/241,040
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,058
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,063
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; PRIOR APPLICATION NUMBER: 60/242,611
; PRIOR FILING DATE: 2000-10-23
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; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/242,881
; PRIOR FILING DATE: 2000-10-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2997
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (857)..(858)

OTHER INFORMATION: wherein n is an a or t or c or g.
FEATURE:
NAME/KEY: misc feature
LOCATION: (2383)
OTHER INFORMATION: wherein n is an a or t or c or g.
FEATURE:
NAME/KEY: misc feature
LOCATION: (2983)
OTHER INFORMATION: wherein n is an a or t or c or g.
US-09-981-151A-1

Query Match 92.4%; Score 2675.4; DB 10; Length 2997;
Best Local Similarity 94.9%; Pred. No. 0;
Matches 2866; Conservative 0; Mismatches 5; Indels 150; Gaps 4;

QY 1 CGCTCCTGATGAAGCCCCCGCGCGGATGGCGGGGCTTGGCGGCGCTGTGATGCTG 60
DB 1 CGCTCCTGATGAAGCCCCCGCGCGGATGGCGGGGCTTGGCGGCGCTGTGATGCTG 60
QY 61 TTGGCGCAGGTGGCCGAGCAGAGGTAGTCCCGGGGCTCCCAACGCGGAAACCGGG 120
DB 61 TTGGCGCAGGTGGCCGAGCAGAGGTAGTCCCGGGGCTCCCAACGCGGAAACCGGG 120
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QY 301 AAAGGGCGGACATGATGAAGTGAAGCAACCATGTTCTCAGCAAACTAACACAGGAACA 360
DB 301 AAAGGGCGGACATGATGAAGTGAAGCAACCATGTTCTCAGCAAACTAACACAGGAACA 360
QY 361 GAAAAACCAACACTGCATGTTCTCACTCAATATGACCTGCTCTGCTTCCAGAGTTGAC 420
DB 361 GAAAAACCAACACTGCATGTTCTCACTCAATATGACCTGCTCTGCTTCCAGAGTTGAC 420
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DB 421 CACAGGGCGGATTAAGTGTCCCATGAATCATGCAACCATCAGCGGCGGAAGAGCAAGTG 480
QY 481 GCCGTGTCCGAGGTGAGTGTCTTTCACCTTGGGCTGAAAGGCCCAAGGCAAGCTTCCAC 540
DB 481 GCCGTGTCCGAGGTGAGTGTCTTTCACCTTGGGCTGAAAGGCCCAAGGCAAGCTTCCAC 540
QY 541 ATGATCTGAGGACTTCCAGCAGCCTAGTGCGTCTGCTTTATTGTGACAGCTTGGGA 600
DB 541 ATGATCTGAGGACTTCCAGCAGCCTAGTGCGTCTGCTTTATTGTGACAGCTTGGGA 600
QY 601 AAGACAGGCACTAAGTCTGTGCAAGCTTTACCGCGCAGAGACTTCTGTTTCTATCAAGGC 660
DB 601 AAGACAGGCACTAAGTCTGTGCAAGCTTTACCGCGCAGAGACTTCTGTTTCTATCAAGGC 660
QY 661 TCTTTGCGATCACAGAAATCTGCCATGCGATGGAGGGAAGTTCTGTAGGGCTCCACT 720
DB 661 TCTTTGCGATCACAGAAATCTGCCATGCGATGGAGGGAAGTTCTGTAGGGCTCCACT 720
QY 721 CGCACTCTGAAGCTCTGCAACAGTCAAAATGTCCCGGAGACAGTGTGACTTCCGTGCT 780
DB 721 CGCACTCTGAAGCTCTGCAACAGTCAAAATGTCCCGGAGACAGTGTGACTTCCGTGCT 780
QY 781 GCTCAGTGTGCGAGCACAAACAGCAGAGATTCAAGGGCGGCACTAACAGTGAAGCCT 840
DB 781 GCTCAGTGTGCGAGCACAAACAGCAGAGATTCAAGGGCGGCACTAACAGTGAAGCCT 840
QY 841 TACACTCAAGTAGAAGCCGACTTATGCAAACTCTACTGTATCGCAAGAGATTGATTC 900
DB 841 TACACTCAAGTAGAAGCCGACTTATGCAAACTCTACTGTATCGCAAGAGATTGATTC 900

DB 841 TACACTCAAGTAGAAGNNGACTTATGCAAACTCTACTGTATCGCAAGAGATTGATTC 900
QY 901 TTCTTTTCTTGTCAAAATAAGTCAAAAGATGGGACTCCATGCTCGAGAGATAGCCGTAAT 960
DB 901 TTCTTTTCTTGTCAAAATAAGTCAAAAGATGGGACTCCATGCTCGAGAGATAGCCGTAAT 960
QY 961 GTTTGTATAGATGGAGATATGTAGCTGAGTGTGTGTCACATCTGCGACATGCCCCAG 1020
DB 961 GTTTGTATAGATGGAGATATGTAGCTGAGTGTGTGTCACATCTGCGACATGCCCCAG 1020
QY 1021 CCTCCAAAGGAAGACCTTCTCATCTTGCAGATGATGAATTAAGTCTTTCGATTAAGCGCATTAAG 1080
DB 1021 CCTCCAAAGGAAGACCTTCTCATCTTGCAGATGATGAATTAAGTCTTTCGATTAAGCGCATTAAG 1080
QY 1081 CGCTCTTCTGAGTCCCATAGAATGAAGAACTGAACGTGAGACCTTGTGTGCTC 1140
DB 1081 CGCTCTTCTGAGTCCCATAGAATGAAGAACTGAACGTGAGACCTTGTGTGCTC 1140
QY 1141 GACAAAAAGATGATGCAAAACCATGGCCATGAATAATCAACCTACGTGCTCAGATA 1200
DB 1141 GACAAAAAGATGATGCAAAACCATGGCCATGAATAATCAACCTACGTGCTCAGATA 1200
QY 1201 CTCAACATGCTATCTGCTTATTCAAGA----- 1229
DB 1201 CTCAACATGCTATCTGCTTATTCAAGAATGAACAATAAGAGAAACATCAACATTTGCA 1260
QY 1230 ----- 1229
DB 1261 ATTGAGTCTGATTCTTCTAGAAGATGAACAGCCAGACTGTGATTAAGTCAACACGCA 1320
QY 1230 -----TGATTTGATGGGAAAGATGGGACT 1254
DB 1321 GACCACACTTAAGTAGCTTCTGCCAGTGGCAGTCTGATTTGATGGGAAAGATGGGACT 1380
QY 1255 GGTATGACCAAGCCATCTTACTGACTGTCTGATTAATGTTCTCTGGAAGATGAGCCC 1314
DB 1381 GGTATGACCAAGCCATCTTACTGACTGTCTGATTAATGTTCTCTGGAAGATGAGCCC 1440
QY 1315 TGTGACACTTTGGATTTGACCCCAATAAGTGAATGTGTAATAATTCGACGTGCAG 1374
DB 1441 TGTGACACTTTGGATTTGACCCCAATAAGTGAATGTGTAATAATTCGACGTGCAG 1500
QY 1375 ATTAATGAAGATACAGGCTTTGACTGGCTTACCAATGCCCCATGAGTCTGGACACAAC 1434
DB 1501 ATTAATGAAGATACAGGCTTTGACTGGCTTACCAATGCCCCATGAGTCTGGACACAAC 1560
QY 1435 TTTGCAATGATTATGATGAGAAAGGAACATGTGTAAAAAGTCCGAGGGCAACATCATG 1494
DB 1561 TTTGCAATGATTATGATGAGAAAGGAACATGTGTAAAAAGTCCGAGGGCAACATCATG 1620
QY 1495 TCCCTTACATTTGGCAGAGCGCAATGAGTCTTCTCTGTGTCACCTGAGCCGCAAGTAT 1554
DB 1621 TCCCTTACATTTGGCAGAGCGCAATGAGTCTTCTCTGTGTCACCTGAGCCGCAAGTAT 1680
QY 1555 CTACACAAATTTCTAAGCACCCTCAAGCTATCTGCTGTGATCAGCCAAAGCCTGTG 1614
DB 1681 CTACACAAATTTCTAAGCACCCTCAAGCTATCTGCTGTGATCAGCCAAAGCCTGTG 1740
QY 1615 AAGGAATCAAGTATCTTGAGAAATTGCGCAGAGAAATTATATGATGCAAAACACACAGTGC 1674
DB 1741 AAGGAATCAAGTATCTTGAGAAATTGCGCAGAGAAATTATATGATGCAAAACACAGTGC 1800
QY 1675 AAGTGAGTTTGGAGAGAAAGCCAAAGCTCTGCATGCTGGACTTTAAAAAGACATCTGT 1734
DB 1801 AAGTGAGTTTGGAGAGAAAGCCAAAGCTCTGCATGCTGGACTTTAAAAAGACATCTGT 1860
QY 1735 AAAGCCCTGTGTGCAATCGTATTGGAAGAAATGTGAGACTAAATTTATGCCAGCAGCA 1794
DB 1861 AAAGCCCTGTGTGCAATCGTATTGGAAGAAATGTGAGACTAAATTTATGCCAGCAGCA 1920
QY 1795 GAAGGCAATTTGTGGCATGACATGTGTGCGGGGAGGACAGTGTGTAATATGTG 1854
DB 1921 GAAGGCAATTTGTGGCATGACATGTGTGCGGGGAGGACAGTGTGTAATATGTG 1980

QY	1855	GATGAAGGCCCCAAAGCCCAACCCATGGCACTGGTCGGACTGGTCTTCTTGGTCCCATGC	1914
Db	1981	GATGAAGGCCCCAAAGCCCAACCCATGGCACTGGTCGGACTGGTCTTCTTGGTCCCATGC	2040
QY	1915	TCCAGGACCTCGCGAGGGGGGAGTATCTCATATGAGTGCCTCTGCACCAACCCAAAGCCA	1974
Db	2041	TCCAGGACCTCGCGAGGGGGGAGTATCTCATATGAGTGCCTCTGCACCAACCCAAATCCA	2100
QY	1975	TCGCATGAGAGGAAGTTCTGTGAGGGGCTCCACTTCGCACCTGGAAGCTCTGCAACAGTCAG	2034
Db	2101	TCGCATGAGAGGAAGTTCTGTGAGGGGCTCCACTTCGCACCTGGAAGCTCTGCAACAGTCAG	2160
QY	2035	AAATGTCCCCCGGGAAGAGTTGACTTCCGTGCTGCTCAGTGTGCCGAGCAACAAGCAGA	2094
Db	2161	AAATGTCCCCCGGGAAGAGTTGACTTCCGTGCTGCTCAGTGTGCCGAGCAACAAGCAGA	2220
QY	2095	CGATTCAAGAGGGCGGCACCTACAAGTGGAAAGCCTTACACTCAAAGTAAAGATCAGGACTTA	2154
Db	2221	CGATTCAAGAGGGCGGCACCTACAAGTGGAAAGCCTTACACTCAAAGTAAAGATCAGGACTTA	2262
QY	2155	TGCAAACTCTACTGTATCGCAGAAAGATTGATTTCTTCTTTCTTGTCAATAAAGTC	2214
Db	2263	TGCAAACTCTACTGTATCGCAGAAAGATTGATTTCTTCTTTCTTGTCAATAAAGTC	2322
QY	2215	AAAGATGGGACTCCATGCTCGGAGGATAGCCGTAATGTTGTAATAGATGGATATGTGAG	2274
Db	2323	AAAGATGGGACTCCATGCTCGGAGGATAGCCGTAATGTTGTAATAGATGGATATGTGAG	2382
QY	2275	AGAGTTGATGTGACAAATGTCCTTGGATCTGATGCTGTGTGAAGACGCTGTGGGGTGTGT	2334
Db	2383	---NTTGATGTGACAAATGTCCTTGGATCTGATGCTGTGTGAAGACGCTGTGGGGTGTGT	2439
QY	2335	AAACGGGAATTACTCAGCCTGCACGATTCAACAGGGGTCTCTACACCAAGCACCAACACC	2394
Db	2440	AAACGGGAATTACTCAGCCTGCACGATTCAACAGGGGTCTCTACACCAAGCACCAACACC	2499
QY	2395	AAACGATATTAACAATGTCACCAATTCCTTCTGGAGACCCGGAGTATCCGCATCTATGAA	2454
Db	2500	AAAC---ATTATCAATGTCACCAATTCCTTCTGGAGACCCGGAGTATCCGCATCTATGAA	2556
QY	2455	ATGAACGTCTTAACCTCCTACAATTTCTGTGCGCAATGCCCTGAGAAAGTACTTAACCTGAAT	2514
Db	2557	ATGAACGTCTTAACCTCCTACAATTTCTGTGCGCAATGCCCTGAGAAAGTACTTAACCTGAAT	2616
QY	2515	GGGCACTGACCGTGGACTGGCCCGGCGGTAACAATTTTGGGGCACTACTTTCGACTAC	2574
Db	2617	GGGCACTGACCGTGGACTGGCCCGGCGGTAACAATTTTGGGGCACTACTTTCGACTAC	2676
QY	2575	AGACGGTCTTAATATGAGCCCGAAGACTTAATCGCTACTGGAACCAACCAAGACACTG	2634
Db	2677	AGACGGTCTTAATATGAGCCCGAAGACTTAATCGCTACTGGAACCAACCAAGACACTG	2736
QY	2635	ATTGTGAGCTGCTGTTTCAAGGAAGAAACCCGGGTGTTGCTCGGAATATCTCATGCGCT	2694
Db	2737	ATTGTGAGCTGCTGTTTCAAGGAAGAAACCCGGGTGTTGCTCGGAATATCTCATGCGCT	2796
QY	2695	CGCTTGGGACCGAAGACAGCCCCCTGCCCAGCCCCAGCTACACTTGGGCCATCGTGGC	2754
Db	2797	CGCTTGGGACCGAAGACAGCCCCCTGCCCAGCCCCAGCTACACTTGGGCCATCGTGGC	2856
QY	2755	TCTGAGTGTCCGTGTCCTGCGGAGGGGGTAGGTGCTTCCAGTGTGCTGCTCCGAGAGCA	2814
Db	2857	TCTGAGTGTCCGTGTCCTGCGGAGGGGGTAGGTGCTTCCAGTGTGCTGCTCCGAGAGCA	2916
QY	2815	GCATGTCAAGCTTCAAGCCACTGCGTACATTGCACTGGCCTTCTTGAATCCTAATGAGCA	2874
Db	2917	GCATGTCAAGCTTCAAGCCACTGCGTACATTGCACTGGCCTTCTTGAATCCTAATGAGCA	2976
QY	2875	GCCCCGGGCTTCTCCCTGCCA 2895	
Db	2977	GCCCCGGGCTTCTCCCTGCCA 2997	

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RESULT 3
US-10-330-176-1
; Sequence 1, Application US/10330176
; Publication No. US20030228676A1
; GENERAL INFORMATION:
; APPLICANT: Agostino, Michael
; APPLICANT: DiBlasio, Elizabeth
; TITLE OF INVENTION: AGGREGANASE MOLECULES
; FILE REFERENCE: AM100884
; CURRENT APPLICATION NUMBER: US/10/330,176
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: 60/344,895
; PRIOR FILING DATE: 2001-12-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 3675
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-176-1

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Query Match	64.9%	Score 1877.8	DB 17	Length 3675
Best Local Similarity	84.4%	Pred. No. 0		
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QY	202	GCAGGCACTGCGTGGCCCATGGGACC	CGGACGGCCTGGAGCCCGAGCGTCC	261
Db	69	GCAGGCACTGCGTGGCCCATGGGACC	CGGACGGCCTGGAGCCCGAGCGTCC	128
QY	262	GCGTCTCTCTCCACCCGCGGAGCGG	CCGGGCTGGATGGAAGGGCCGGACAT	321
Db	129	GCGTCTCTCTCCACCCGCGGAGCGG	CCGGGCTGGATGGAAGGGCGC	175
QY	322	GCTGGAACCATCGTCTCAGCAAACT	AACACAGGAACGAAAAACCAACACT	381
Db	176	-----	-----	175
QY	382	CTCACTCAATATGACCTGGTCTCTG	CCCTACGAGTTGACCAAGGGCCATT	441
Db	176	-----AATATGACCTGGTCTCTG	CCCTACGAGTTGACCAAGGGCCATT	228
QY	442	CATGAATATATGACCATCAGCCGGG	AGAGAGAGCAGTGGCCGTCCGAGGT	501
Db	229	CATGAATATATGACCATCAGCCGGG	AGAGAGAGCAGTGGCCGTCCGAGGT	288
QY	502	CTTCACTTGGGCTGAAAGCCCCAGG	CAAGCACTTCCACATGATCTGAGACT	561
Db	289	CTTCACTTGGGCTGAAAGCCCCAGG	CAAGCACTTCCACATGATCTGAGACT	348
QY	562	AGCCTAGTGGCTCTGCTTTATTTG	TGCAACCTTGGGAAAGACAGGCACT	621
Db	349	AGCCTAGTGGCTCTGCTTTATTTG	TGCAACCTTGGGAAAGACAGGCACT	408
QY	622	CAGACTTTACCGCCAGAGGACTTCT	GTTCTATCAAGGCTCTTGGCATCA	681
Db	409	CAGACTTTACCGCCAGAGGACTTCT	GTTCTATCAAGGCTCTTGGCATCA	468
QY	682	TGCGCATCGCATGAGGGAAGTTCTG	TGAGGGCTCCACTCGCACTGGAAG	741
Db	469	TCCTCA-----	GTGGCCCTTCAACCTGCCAAGCTT	504
QY	742	AGTCAGAAATGTCCCGGGAAGTGTG	ACTTCCGTGCTCAGTGTGCCGAGCA	801
Db	505	GGCATGATAGGAACAGAAAGGAGAT	TACTTCCCTAAGGCCACTTCCACAC	564
QY	802	AGCAGACGATTACAGAGGGCGGCA	CTACAAGTGG--AAGCCTTACACT	859
Db	565	TGGAACCTCGGCGAGAGCTGCCCA	AGGCAAGCTGCCCATCCACGTACT	624
QY	860	ACTTATGCAAACTTACTGATCGCA	GAAGGATTGATTTCTTTCTTTGT	919
Db	625	ACAGAGCCCATGCTCTCTGGGGCC	AGTAGGCTCTGATGACCTC-----	672

QY	920	AAATCAAAAGATGGGACTCCATGCTTCGGAGGATAGCCGTAATGTTTGTATAGATGGGATAT	979
Db	673	ACATGGGAGGCTGGGACATCAACCCCTGCACAGCAGCCGACCTTGCCCTGGGACTGCCACAA	732
QY	980	GTCAGCTCAGTGTGTGTGTCCACATCTGC-GCACATGCCCGAGCTCCCAAGAGAAGACCTC	1038
Db	733	AAGCAGCATTTCTGTGGGAAGACCGAAGAAATATACATGCCAGCCTCCCAAGGAAGACCTC	792
QY	1039	TTTCATCTTGGCCAGATGAGTATAAGTCTTGCTTACGGCATTAAGGCGCTCTTCTGAGGTCC	1098
Db	793	TTTCATCTTGGCCAGATGAGTATAAGTCTTGCTTACGGCATTAAGGCGCTCTTCTGAGGTCC	852
QY	1099	CATAGAAATGAAGAACTGAAACGTGGAGACCTTGSTGTGTGTCACAAAAGATGATGCAA	1158
Db	853	CATAGAAATGAAGAACTGAAACGTGGAGACCTTGSTGTGTGTCACAAAAGATGATGCAA	912
QY	1159	AACCATGGCCATGAAAAATATCACCACTACGTGCTCACGATCTCAACATGTTATCTGCT	1218
Db	913	AACCATGGCCATGAAAAATATCACCACTACGTGCTCACGATCTCAACATGTTATCTGCT	972
QY	1219	TTTATTCAAAGA-----	1229
Db	973	TTTATTCAAAGATGGAACAATAGGAGAAACATCAATTGCAATTGTAGTCTGATTCTT	1032
QY	1230	-----	1229
Db	1033	CTAGAAAGATGAACAGCCAGGACTGTGTGATTAAGTCAACCAAGCAGACCAACCTTAAAGTAGC	1092
QY	1230	-----TGATTGATGGGGAAGATGGGACTCTGTCTATGACACGCCATC	1272
Db	1093	TTCTGCCAGTGGCAGTCTGGATTGATGGGGAAGATGGGACTCTGTCTATGACACGCCATC	1152
QY	1273	TTTACTGACTGTCTGATATATGTCTCTGGAAGATGAGCCCTGTGACACTTTGGGATTT	1332
Db	1153	TTTACTGACTGTCTGATATATGTCTCTGGAAGATGAGCCCTGTGACACTTTGGGATTT	1212
QY	1333	GCAACCCATTAAGTGAATGTGTAAATATCGCAGCTGCACGATTAATGAAGATACAGGT	1392
Db	1213	GCAACCCATTAAGTGAATGTGTAAATATCGCAGCTGCACGATTAATGAAGATACAGGT	1272
QY	1393	CTTGGACTGGCCTTCAACCATTTGCCCATGAGTCTGGACACAACTTTGGCATGATTCATGAT	1452
Db	1273	CTTGGACTGGCCTTCAACCATTTGCCCATGAGTCTGGACACAACTTTGGCATGATTCATGAT	1332
QY	1453	GGAGAAAGGGAACAATGTGTAAAAAGTCCGAGGGCAACATCATGTCCCTTACATTGGCAGGA	1512
Db	1333	GGAGAAAGGGAACAATGTGTAAAAAGTCCGAGGGCAACATCATGTCCCTTACATTGGCAGGA	1392
QY	1513	CGCAATGGAGTCTTCTCCTGTGTACCCCTGCAGCGCCAGTATCTACACAAAATTTCTAAGC	1572
Db	1393	CGCAATGGAGTCTTCTCCTGTGTACCCCTGCAGCGCCAGTATCTACACAAAATTTCTAAGC	1452
QY	1573	ACCGCTCAAGCTATCTGCCTTGTGTATCAGCCAAAGCCTGTGAAGGAATACAAATATCTCT	1632
Db	1453	ACCGCTCAAGCTATCTGCCTTGTGTATCAGCCAAAGCCTGTGAAGGAATACAAATATCTCT	1512
QY	1633	GAGAAATTGCCAGGAGAAATTATATGATGCAAAACACACAGTGCAGAGTGCGAGGAG	1692
Db	1513	GAGAAATTGCCAGGAGAAATTATATGATGCAAAACACACAGTGCAGAGTGCGAGGAG	1572
QY	1693	AAAAGCCAAAGCTCTGCATGCTGGAATTAAAAAGGACATCTGTAAAGCCCTGTGTGCCAT	1752
Db	1573	AAAAGCCAAAGCTCTGCATGCTGGAATTAAAAAGGACATCTGTAAAGCCCTGTGTGCCAT	1632
QY	1753	CGTATTGGAAGGAATGTGAGACTAAATTTATGCCCAGCAGAGAAAGGACAAATTTGTGGG	1812
Db	1633	CGTATTGGAAGGAATGTGAGACTAAATTTATGCCCAGCAGAGAAAGGACAAATTTGTGGG	1692
QY	1813	CATGACATGTGTGCCGGGGAGGACAGTGTGTGAATAATGTGTATGAAGGCCCAAGGCC	1872
Db	1693	CATGACATGTGTGCCGGGGAGGACAGTGTGTGAATAATGTGTATGAAGGCCCAAGGCC	1752

QY	1873	ACCCATGGCCACTGGTCGGACCTGGTCTTCTTGGTCCCATGCTCCAGGACCTGCCGAGGG	1932
Db	1753	ACCCTATGGCCACTGGTCGGACCTGGTCTTCTTGGTCCCATGCTCCAGGACCTGCCGAGGG	1812
QY	1933	GGAGTATCTCAATAGGAGTCGCGCTCTGCACCAACCCCAAGCCATCGCATGGAGGAATTTC	1992
Db	1813	GGAGTATCTCAATAGGAGTCGCGCTCTGCACCAACCCCAAGCCATCGCATGGAGGAATTTC	1872
QY	1993	TGTGAGGGGCTCCACTCGCACTCTGAAAGCTCTGCACAAGTCAAGAAATGTCCCCGGGACAGT	2052
Db	1873	TGTGAGGGGCTCCACTCGCACTCTGAAAGCTCTGCACAAGTCAAGAAATGTCCCCGGGACAGT	1932
QY	2053	GTTGACTTCCGCTGCTGCTCAAGTGTGCCGAGCAACAAGCAGACGATTCAGAGGGCGGCAC	2112
Db	1933	GTTGACTTCCGCTGCTGCTCAAGTGTGCCGAGCAACAAGCAGACGATTCAGAGGGCGGCAC	1992
QY	2113	TACAAGTGAAGCCTTACACTCAAGTAGAAGATCAGGACTTATGCAAACTCTACTGTATC	2172
Db	1993	TACAAGTGAAGCCTTACACTCAAGTAGAAGATCAGGACTTATGCAAACTCTACTGTATC	2052
QY	2173	GCAGAAGGATTTGATTTCTTCTTTCTTTGTCAATTAAGTCAAAAGTGGAGCTCCATGC	2232
Db	2053	GCAGAAGGATTTGATTTCTTCTTTCTTTGTCAATTAAGTCAAAAGTGGAGCTCCATGC	2112
QY	2233	TCGGAGATAGCCGTAATGTTGTATAGATGGATATGTGAGAGATTGGATGTGCAAT	2292
Db	2113	TCGGAGATAGCCGTAATGTTGTATAGATGGATATGTGAGAGATTGGATGTGCAAT	2172
QY	2293	GTCCTTGATCTGATGCTGTGTAAGACGTCGTGGGGGTGTGTAACGGGAATTAATCAGCC	2352
Db	2173	GTCCTTGATCTGATGCTGTGTAAGACGTCGTGGGGGTGTGTAACGGGAATTAATCAGCC	2232
QY	2353	TGCACGATTCACAGGGGTCTCTACACCAAGCACCAACACACCAACCAAGTATTATCATG	2412
Db	2233	TGCACGATTCACAGGGGTCTCTACACCAAGCACCAACACACCAACCAAGTATTATCATG	2292
QY	2413	GTCACCAATTCCTTCTGAGCCCGGAGTATCCGCATCTATGAAATGAACGTCCTACCTCC	2472
Db	2293	GTCACCAATTCCTTCTGAGCCCGGAGTATCCGCATCTATGAAATGAACGTCCTACCTCC	2352
QY	2473	TACATTTCTGTGCGCAATGCCCTCAGAAAGTACTACCTGAATGGGCACTGGAACCTGGAC	2532
Db	2353	TACATTTCTGTGCGCAATGCCCTCAGAAAGTACTACCTGAATGGGCACTGGAACCTGGAC	2412
QY	2533	TGGCCCGGCGGTACAAATTTTTCGGGCACCTATTTCGACTACAGACGGTCCCTATTAATGAG	2592
Db	2413	TGGCCCGGCGGTACAAATTTTTCGGGCACCTATTTCGACTACAGACGGTCCCTATTAATGAG	2472
QY	2593	CCCGAAGAACTTAATCGCTACTGGAACCAACCAAGAGACACTGAATTGTGAGCTGCTGTTT	2652
Db	2473	CCCGAAGAACTTAATCGCTACTGGAACCAACCAAGAGACACTGAATTGTGAGCTGCTGTTT	2532
QY	2653	CAGGGAAGAACCCGGGTGTGCTTGGAATACTCCATGCTTCGCTTGGGGACCGAAG	2712
Db	2533	CAGGGAAGAACCCGGGTGTGCTTGGAATACTCCATGCTTCGCTTGGGGACCGAAG	2592
QY	2713	CAGCCCTGCTGCCAGCCCAAGTACACTTGGGCCATCGTGCCTCTGAGTGTCCGTGTCC	2772
Db	2593	CAGCCCTGCTGCCAGCCCAAGTACACTTGGGCCATCGTGCCTCTGAGTGTCCGTGTCC	2652
QY	2773	TGCGGAGGGGG 2783	
Db	2653	TGCGGAGGGGG 2663	

RESULT 4
US-10-275-107-16
; Sequence 16, Application US/10275107
; Publication No. US20040063107A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY D.
; APPLICANT: WHYTE, DAVID
; APPLICANT: SUDARSANAM, SUCHA

QY 1039 TTTCATCTTGCCAGATGAGTATTAAGTCTTGCTTACGGCATTAAGCGCTCTTCTGAGGTCC 1098
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Db 793 TTTCATCTTGCCAGATGAGTATTAAGTCTTGCTTACGGCATTAAGCGCTCTTCTGAGGTCC 852
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QY 1099 CATAGAAATGAAGAACTGAAACGTGAGAACCTTGCTGCTGCTGCACAAAAAGATGATGCAA 1158
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Db 913 AACCATGGCCATGAAAATATCAACCACTACGTGCTCAACGATCTCAACATGATCTGCT 972
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QY 1219 TTATTCAAAGA----- 1229
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Db 973 TTATTCAAAGATGGAAACAATAGAGGAAACATCAATTGCAATTGTAGTCTGATTCTT 1032
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QY 1230 ----- 1229
| | | | |
Db 1033 CTAGAAAGATGAACAGCCAGACTGGTGATAGTCAACAGCAGACCAACCTTAAGTAGC 1092
| | | | |
QY 1230 -----TGGATTGATGGGGAAGATGGGACTCGTCATGACCAAGCCATC 1272
| | | | |
Db 1093 TTCTGCCAGTGGCAGTCTGGATTGATGGGGAAGATGGGACTCGTCATGACCAAGCCATC 1152
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QY 1273 TTTACTGACTGCTGCTGATATATGTTCTCTGGAAGAAATGAGCCCTGTGACACTTTGGGATTT 1332
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Db 1153 TTTACTGACTGCTGCTGATATATGTTCTCTGGAAGAAATGAGCCCTGTGACACTTTGGGATTT 1212
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QY 1333 GCACCCCATAGTGGAATGTGTAAATATCGCAGCTGCACCGATTAAATGAAGATACAGGT 1392
| | | | |
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Db 1273 CTTGGACTGGCTTCAACCATTTGCCATGAGTCTGGAACACAACTTTGGCATGATTCATGAT 1332
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| | | | |
Db 1573 AAAGCCCAAGCTCTGCACTGCTGCACTTTAAAAAGGACATCTGTAAAGCCCTGTGCTCCAT 1632
| | | | |
QY 1753 CGTATTGGAAGAAATGTGAGACTAAATTATGCAAGCAGCAGAGGACAAATTTGTGGG 1812
| | | | |
Db 1633 CGTATTGGAAGAAATGTGAGACTAAATTATGCAAGCAGCAGAGGACAAATTTGTGGG 1692
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| | | | |
Db 1693 CATGACATGTGTGCGCGGGAGAGCAGTGTGAAATATGTGATGAAGGCCCAAGCCC 1752
| | | | |
QY 1873 ACCCATGGCCACTGGTTCGGAATGCTTCTTGTGCTCCCATGCTCCAGGACTGCGAGGG 1932
| | | | |
Db 1753 ACCCATGGCCACTGGTTCGGAATGCTTCTTGTGCTCCCATGCTCCAGGACTGCGAGGG 1812
| | | | |
QY 1933 GAGATATCTCATAGAGAGTGCCTCTGCAACCAACCCCAAGCCATGCAATGAGGAAAGTTTC 1992
| | | | |
Db 1813 GAGATATCTCATAGAGAGTGCCTCTGCAACCAACCCCAAGCCATGCAATGAGGAAAGTTTC 1872
| | | | |
QY 1993 TGTGAGGGCTCCTCACTCGCACTCTGAAGCTCTGCAACAGTCAGAAATGTCCCCGGGACAGT 2052
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Db 1873 TGTGAGGGCTCCTCACTCGCACTCTGAAAGCTCTGCAACAGTCAGAAATGTCCCCGGGACAGT 1932
| | | | |
QY 2053 GTTGACTTCCTGCTGCTCAGTGTGCGGAGACCAACAGCAGACGATTTCAGAGGGCGGCAC 2112
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Db 1933 GTTGACTTCCTGCTGCTCAGTGTGCGGAGACCAACAGCAGACGATTTCAGAGGGCGGCAC 1992
| | | | |
QY 2113 TACAAGTGAAGCCTTACACTCAAGTAGAAGATCAAGACTTATGCAAACTCTACTGTATC 2172
| | | | |
Db 1993 TACAAGTGAAGCCTTACACTCAAGTAGAAGATCAAGACTTATGCAAACTCTACTGTATC 2052
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QY 2173 GCAGAAAGATTGATTCTTCTTCTTCTTGTGCAATTAAGTCAAAAGATGGGACTCCATGC 2232
| | | | |
Db 2053 GCAGAAAGATTGATTCTTCTTCTTCTTGTGCAATTAAGTCAAAAGATGGGACTCCATGC 2112
| | | | |
QY 2233 TCGGAGGATAGCCGTAATGTTGTATAGATGGGATATGTGAGAGAGTTGATGTGACAAAT 2292
| | | | |
Db 2113 TCGGAGGATAGCCGTAATGTTGTATAGATGGGATATGTGAGAGAGTTGATGTGACAAAT 2172
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QY 2293 GTCTTGGATCTGATGCTGTGGAAGACGCTGTGGGGTGTGTAAAGGGAATTAACAGCC 2352
| | | | |
Db 2173 GTCTTGGATCTGATGCTGTGGAAGACGCTGTGGGGTGTGTAAAGGGAATTAACAGCC 2232
| | | | |
QY 2353 TGCAAGATTACAGGGGTCTCTACACCAAGCACCAACCAACAGATTAATCAATG 2412
| | | | |
Db 2233 TGCAAGATTACAGGGGTCTCTACACCAAGCACCAACCAACAGATTAATCAATG 2292
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QY 2413 GTCAACATTCTTCTGAGCCCGAGATATCCGATCTATGAATGAACGTCTCTACCTCC 2472
| | | | |
Db 2293 GTCAACATTCTTCTGAGCCCGAGATATCCGATCTATGAATGAACGTCTCTACCTCC 2352
| | | | |
QY 2473 TACATTCTGTGCGCAATGCGCTCAGAAAGTAATCCTGAATGGGCACTGGAACCGTGAC 2532
| | | | |
Db 2353 TACATTCTGTGCGCAATGCGCTCAGAAAGTAATCCTGAATGGGCACTGGAACCGTGAC 2412
| | | | |
QY 2533 TGGCCCGCGCGTACAATTTTCGGGCACTACTTTCGACTACAGACGCTCTTAATGAG 2592
| | | | |
Db 2413 TGGCCCGCGCGTACAATTTTCGGGCACTACTTTCGACTACAGACGCTCTTAATGAG 2472
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QY 2593 CCCGAACTTAATCGCTACTGGAACCAACCAAGAGACATGATGTGAGCTGCTGTTT 2652
| | | | |
Db 2473 CCCGAACTTAATCGCTACTGGAACCAACCAAGAGACATGATGTGAGCTGCTGTTT 2532
| | | | |
QY 2653 CAGGGAAGAACCCGGGTGCTGCGGAAATCTCCATGCTCTGCGGACCGAGAAAG 2712
| | | | |
Db 2533 CAGGGAAGAACCCGGGTGCTGCGGAAATCTCCATGCTCTGCGGACCGAGAAAG 2592
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QY 2713 CAGCCCTGCGCCAGCCCACTACACTTGGGCACTGCGCTCTGAGTGTCCGTGTC 2772
| | | | |
Db 2593 CAGCCCTGCGCCAGCCCACTACACTTGGGCACTGCGCTCTGAGTGTCCGTGTC 2652
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QY 2773 TGCGGAGGGGG 2783
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Db 2653 TGCGGAGGGGG 2663
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RESULT 6
US-10-296-616-1
; Sequence 1, Application US/10296616
; Publication No. US20030129658A1
; GENERAL INFORMATION:
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: No. US20030129658A1e1 protease
; FILE REFERENCE: Y0132PCT-664
; CURRENT APPLICATION NUMBER: US/10/296,616
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: JP 2000-393372
; PRIOR FILING DATE: 2000-12-25
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 1
; LENGTH: 3675
; TYPE: DNA
; ORGANISM: Homo sapiens

FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3675)
US-10-296-616-1

Query Match 64.8%; Score 1874.6; DB 15; Length 3675;
Best Local Similarity 84.4%; Pred. No. 0;
Matches 2287; Conservative 0; Mismatches 179; Indels 245; Gaps 6;

QY	202	GCAGGACCTGCGTGGCCCATGGGACCCGACGGCGAGCCCTGGGAGCCCGAGCGTCCC	261
DB	69	GCAGGACCTGCGTGGCCCATGGGACCCGACGGCGAGCCCTGGGAGCCCGAGCGTCCC	128
QY	262	GCGTCTCTCCACCCCGGAGCGCGCGGCTGGATGGAAAAGCGGGACATGGATGAA	321
DB	129	GCGTCTCTCTCCACCCCGGAGCGCGCGGCTGGATGGAAAAGCGG-----	175
QY	322	GCTGGAACCATCGTTCTCAGCAAACTAACAGGAACGAAAACCAACACTGCATGTT	381
DB	176	-----	175
QY	382	CTCACTCAATATGACCTGTCTCTGCTTACGAGTTGACCAACAGGGCGATTACGTGTC	441
DB	176	-----AATATGACCTGTCTCTGCTTACGAGTTGACCAACAGGGCGATTACGTGTC	228
QY	442	CATGAATATCATGCCATCAGCGCGGAGAGAAGCAGTGGCGCTGTCCGAGTTGAGTCT	501
DB	229	CATGAATATCATGCCATCAGCGCGGAGAGAAGCAGTGGCGCTGTCCGAGTTGAGTCT	288
QY	502	CTTCACTTGGGCTGAAAGGCCCGAGGACGACTTCCACATGGATCTGAGGACTTCCAGC	561
DB	289	CTTCACTTGGGCTGAAAGGCCCGAGGACGACTTCCACATGGATCTGAGGACTTCCAGC	348
QY	562	AGCCTAGTGGCTCTGCTTTATTTGTGACAGCTTGGGAAAAGCAGGCACTAAGTCTGTG	621
DB	349	AGCCTAGTGGCTCTGCTTTATTTGTGACAGCTTGGGAAAAGCAGGCACTAAGTCTGTG	408
QY	622	CAGACTTTACCGCCAGAGGACTTCTGTTCTATCAAGGCTCTTTGGATCACACAGAAAC	681
DB	409	CAGACTTTACCGCCAGAGGACTTCTGTTCTATCAAGGCTCTTTGGATCACACAGAAAC	468
QY	682	TCGCCATCGCATGGAGGGAATTCTGTGAGGGCTCCACTCGCACTGGAAGCTCTGCAAC	741
DB	469	TCCTCA-----GTGGCCCTTTCAACCTGCCAAGGCTTGTCA	504
QY	742	AGTCAGAAATGTCCCCGGGACAGTGTGACTTCCCTGCTGCTCAGTGTGCCGACACAAC	801
DB	505	GGCATGATACGAACAGAAAGGACGATTACTTCTTAAGGCCACTTCTTACACCTCTCA	564
QY	802	AGCAGACGATTCAAGGGCGGCACTCAAGTGG--AAGCCTTACACTCAAGTAGAAGCCG	859
DB	565	TGGAAACTCGGACAGAGCTGCCCAAGGCACTGCCCATCCACGTACTGTACAAAGATCC	624
QY	860	ACTTATGCAAACTCTACTGTATCGCAGAAAGGATTGATTCTTTCTTTGTCAATA	919
DB	625	ACAGAGCCCCCATGCTCTGCGGCGCACTGAAGTCTGTGACCTC-----AAGG	672
QY	920	AACTCAAAGATGGGACTCCATGCTCGGAGGATAGCCGTAATGTTGTATAGATGGATAT	979
DB	673	ACATGGAGCTGGCACATCAACCTCTGCACAGCAGCGAACCCTTGGCTGGACTGCCACAA	732
QY	980	GTGAGCTCAGTGTGTGTCCACATCTGC-GCACATGCCCCAGGCTCCCAAGGAAGACCTC	1038
DB	733	AAGCAGCATTTCTGTGGAAGCGCAAGAAATACATGCCCCAGCCTCCCAAGGAAGACCTC	792
QY	1039	TTTCATCTTGGCAGATGAGTATTAAGTCTTGTCTTACGGCATTAAGCGCTCTTCTGAGGTC	1098
DB	793	TTTCATCTTGGCAGATGAGTATTAAGTCTTGTCTTACGGCATTAAGCGCTCTTCTGAGGTC	852
QY	1099	CATAGAAATGAAGAACTGAACGTGGAGACCTTGGTGTGTGTCACAAAAAGATGATGCAA	1158
DB	853	CATAGAAATGAAGAACTGAACGTGGAGACCTTGGTGTGTGTCACAAAAAGATGATGCAA	912

QY	1159	AACCATGGCCATGAAAATATCACCACTACGTGCTCAGCATACTCAACATGGTATCTGCT	1218
DB	913	AACCATGGCCATGAAAATATCACCACTACGTGCTCAGCATACTCAACATGGTATCTGCT	972
QY	1219	TTATTCAAAGA-----	1229
DB	973	TTATTCAAAGATGAAACAATAGAGGAAACATCAACATTGCAATTGTAGTCTGATTCTT	1032
QY	1230	-----	1229
DB	1033	CTAGAAATGAACAGCCAGACTGTGTAAAGTCAACCAAGCAGACACACCTTAAGTAGC	1092
QY	1230	-----TGATTGATGGGAAAAGATGGGACTCGTCATGACCAAGCCATC	1272
DB	1093	TTCTGCCAGTGGCAGTCTGGATTGATGGGAAAAGATGGGACTCGTCATGACCAAGCCATC	1152
QY	1273	TTACTGACTGGTCTGGAATATATGTTCTCGGAAGAATGAGCCCTGTGACACTTGGGATTT	1332
DB	1153	TTACTGACTGGTCTGGAATATATGTTCTCGGAAGAATGAGCCCTGTGACACTTGGGATTT	1212
QY	1333	GCACCCATTAAGTGAATGTAGTAATAATCGCAGCTGCACGATTAATGAATACAGGT	1392
DB	1213	GCACCCATTAAGTGAATGTAGTAATAATCGCAGCTGCACGATTAATGAATACAGGT	1272
QY	1393	CTTGAAGTGGCTTACCAATGGCCATGAGTCTGAGACAACTTTGGCAGTTCATGAT	1452
DB	1273	CTTGAAGTGGCTTACCAATGGCCATGAGTCTGAGACAACTTTGGCAGTTCATGAT	1332
QY	1453	GGAGAAAGGAACATGTGTAAAGTCCGAGGGCAACATCATGTCCCCTACATTGGCAGGA	1512
DB	1333	GGAGAAAGGAACATGTGTAAAGTCCGAGGGCAACATCATGTCCCCTACATTGGCAGGA	1392
QY	1513	CGCAATGAGTCTTCTCTGTGTCAACCTGCAGCCGCGCATCTACACAATTTCTAAGC	1572
DB	1393	CGCAATGAGTCTTCTCTGTGTCAACCTGCAGCCGCGCATCTACACAATTTCTAAGC	1452
QY	1573	ACCGCTCAAGCTATCTGCTGTGTGATGACCAAGCCGTGAAGGAATACAAGTATCCT	1632
DB	1453	ACCGCTCAAGCTATCTGCTGTGTGATGACCAAGCCGTGAAGGAATACAAGTATCCT	1512
QY	1633	GAGAAATGGCCAGAGAAATATATGATGCAAAACACAGAGTGAAGTGGCAATTGCGAAG	1692
DB	1513	GAGAAATGGCCAGAGAAATATATGATGCAAAACACAGAGTGAAGTGGCAATTGCGAAG	1572
QY	1693	AAAGCCAAGCTCTGACGTGCTGACTTTAAAGGACATCTGTAAAGCCGTGTGCCAT	1752
DB	1573	AAAGCCAAGCTCTGACGTGCTGACTTTAAAGGACATCTGTAAAGCCGTGTGCCAT	1632
QY	1753	CGTATTGGAAGGAATGAGACTAAATTTATGCCAGACAGAAAGGCAATTTGTGGG	1812
DB	1633	CGTATTGGAAGGAATGAGACTAAATTTATGCCAGACAGAAAGGCAATTTGTGGG	1692
QY	1813	CATGACATGTGTGCGCGGGAGGACAGTGTGTAATAATGTGATGAAGCCCCCAAGCCC	1872
DB	1693	CATGACATGTGTGCGCGGGAGGACAGTGTGTAATAATGTGATGAAGCCCCCAAGCCC	1752
QY	1873	ACCCATGGCCACTGTGCGGACTGTCTTCTTGTGTCCCATGCTCCAGGACCTGCGAGGG	1932
DB	1753	ACCCATGGCCACTGTGCGGAGTGTCTTCTTGTGTCCCATGCTCCAGGACCTGCGAGGG	1812
QY	1933	GAGTATCTCATAGAGTGGCTCTGACCAACCCCAAGCCATCGCATGGAGGAAGTTTC	1992
DB	1813	GAGTATCTCATAGAGTGGCTCTGACCAACCCCAAGCCATCGCATGGAGGAAGTTTC	1872
QY	1993	TGTGAGGGCTCCACTGCGCACTCTGAAGCTCTGCAACAGTCAAGAAATGCCCCGGAGACT	2052
DB	1873	TGTGAGGGCTCCACTGCGCACTCTGAAGCTCTGCAACAGTCAAGAAATGCCCCGGAGACT	1932
QY	2053	GTTGACTTCCGTGCTCAGTGTGCGGAGCACAACAGCAGACGATTCAAGAGGCGGCAAC	2112
DB	1933	GTTGACTTCCGTGCTCAGTGTGCGGAGCACAACAGCAGACGATTCAAGAGGCGGCAAC	1992
QY	2113	TACAAGTGAAGCCTTACACTCAAGTGAAGATCAGGACTTATGCAAACTTACTGTATC	2172

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Db 1993 TACAGTGGAGCCTTACACTCAAGTAGAGATCAGGACTTATGCAAACTCTACTGTATC 2052
QY 2173 GCAGAGGATTTGATTTCTTCTTTCTTTGTGCAATAAAGTCAAAAGATGGAGCTCCATGC 2232
Db 2053 GCAGAGGATTTGATTTCTTCTTTCTTTGTGCAATAAAGTCAAAAGATGGAGCTCCATGC 2112
QY 2233 TCGGAGGATAGCCGTAATGTTGTATAGATGGGATATGTGAGAGAGTTGGATGTGACAAT 2292
Db 2113 TCGGAGGATAGCCGTAATGTTGTATAGATGGGATATGTGAGAGAGTTGGATGTGACAAT 2172
QY 2293 GTCTTGGATCTGATGCTGTGTAAGACGTCTGTGGGGTGTGTAAAGGGAATTAATCAGCC 2352
Db 2173 GTCTTGGATCTGATGCTGTGTAAGACGTCTGTGGGGTGTGTAAAGGGAATTAATCAGCC 2232
QY 2353 TGCAGGATTACAGGGGGTCTCTACACCAAGCACCAACCAACCAAGTATTATCAGATG 2412
Db 2233 TGCAGGATTACAGGGGGTCTCTACACCAAGCACCAACCAACCAAGTATTATCAGATG 2292
QY 2413 GTCAACCATTCCTTCTGAGAGCCCGGAGTATCCGCATCTATGAAATGAACGTCTTAACCTCC 2472
Db 2293 GTCAACCATTCCTTCTGAGAGCCCGGAGTATCCGCATCTATGAAATGAACGTCTTAACCTCC 2352
QY 2473 TACATTTCTGTGCGCAATGCCCTCAGAAAGGTACTAAGTAAATGGCACTGAGCCGTGAC 2532
Db 2353 TACATTTCTGTGCGCAATGCCCTCAGAAAGGTACTAAGTAAATGGCACTGAGCCGTGAC 2412
QY 2533 TGGCCCGGCGGTACAATTTTCGGGCACTACTTTGACTACAGACGGTCCATTAATGAG 2592
Db 2413 TGGCCCGGCGGTACAATTTTCGGGCACTACTTTGACTACAGACGGTCCATTAATGAG 2472
QY 2593 CCGAGAACTTAATCGCTACTGGAACCAACCAAGCACTGATTTGTGAGCTGCTGTTT 2652
Db 2473 CCGAGAACTTAATCGCTACTGGAACCAACCAAGCACTGATTTGTGAGCTGCTGTTT 2532
QY 2653 CAGGGAAGAAACCCGGGTGTGCTGCGGAATATCTCATGCTCGCTTGGGACCGAGAAG 2712
Db 2533 CAGGGAAGAAACCCGGGTGTGCTGCGGAATATCTCATGCTCGCTTGGGACCGAGAAG 2592
QY 2713 CAGCCCCCTGCGCAACCCAGCTACACTTGGGCACTGCGCTGAGTGTCCGTGCTCC 2772
Db 2593 CAGCCCCCTGCGCAACCCAGCTACACTTGGGCACTGCGCTGAGTGTCCGTGCTCC 2652
QY 2773 TCGGAGAGGGG 2783
Db 2653 TCGGAGAGGGG 2663
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RESULT 7

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US-10-804-457-3
; Sequence 3, Application US/10804457
; Publication No. US2005065334A1
; GENERAL INFORMATION:
; APPLICANT: Fiddle, Carl Johan
; APPLICANT: Hilbun, Erin
; TITLE OF INVENTION: Novel Human Proteases and Polynucleotides Encoding the
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0219-USA
; CURRENT APPLICATION NUMBER: US/10/804,457
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US/10/217,774
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US/09/930,872
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,852
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3675
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-804-457-3
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Query Match 64.8%; Score 1874.6; DB 21; Length 3675;
Best Local Similarity 84.4%; Pred. No. 0;
Matches 2287; Conservative 0; Mismatches 179; Indels 245; Gaps 6;

QY 202 GCAGGACCTGGGTGCGCCATGGGAAACCCGACGCGGACGCGCTGGGAGCCCGAGCGTCCC 261
Db 69 GCAGGACCTGGGTGCGCCATGGGAAACCCGACGCGGACGCGCTGGGAGCCCGAGCGTCCC 128
QY 262 GCGTCTCTTCCACCCCGGAGCGGGCGGCTGGATGGAAGGGCGGACATGATGAA 321
Db 129 GCGTCTCTTCCACCCCGGAGCGGGCGGCTGGATGGAAGGGCGG----- 175
QY 322 GCTGAAACCATCGTTCTCAGCAACTAACAAGGAACAGAAACCAAACTGCATGTT 381
Db 176 ----- 175
QY 382 CTCACCTAATATGACCTGGTCTCTGCTTACGAGGTTGACCAAGGGCGATTAAGTGTCC 441
Db 176 -----AATATGACCTGGTCTCTGCTTACGAGGTTGACCAAGGGCGATTAAGTGTCC 228
QY 442 CATGAATCATGCAACCATCAGCGGGGAGAAAGACAGTGGCGGTGCCGAGTTGAGTCT 501
Db 229 CATGAATCATGCAACCATCAGCGGGGAGAAAGACAGTGGCGGTGCCGAGTTGAGTCT 288
QY 502 CTTACACCTTCGGCTGAAGGCGCCAGGACGACTTCCACATGATCTGAGGACTTCCAGC 561
Db 289 CTTACACCTTCGGCTGAAGGCTTCAGGACGACTTCCACATGATCTGAGGACTTCCAGC 348
QY 562 AGCTTAGTGGCTCCTGGCTTTATGTGACAGCGTTGGAAAGACAGGACATAAGTCTGTG 621
Db 349 AGCTTAGTGGCTCCTGGCTTTATGTGACAGCGTTGGAAAGACAGGACATAAGTCTGTG 408
QY 622 CAGACTTTACCGCAGAGGACTTCTGTTTATCAAGGCTTTTGCATCACAAGAAAC 681
Db 409 CAGACTTTACCGCAGAGGACTTCTGTTTATCAAGGCTTTTGCATCACAAGAAAC 468
QY 682 TCGCATCGCATGAGAGGAAGTTCTGTAGGGCTCCACTCGCACTGTGAAGCTCTGCAAC 741
Db 469 TCCTCA-----GTGGCCCTTCAACTGCCAAGGCTTGTCA 504
QY 742 AGTCAGAAATGTCCCGGACAGTGTGACTTCGCTGCTCAGTGTGCCGACACAAC 801
Db 505 GGCATGATACGAACAGAAAGGCAAGTACTTCTTAAGGCCACTTCTTCAACCTCTCA 564
QY 802 AGCAGAGATTCAGAGGGCGGCACTACAAGTGG--AAGCTTACACTCAAGTAGAAGCCG 859
Db 565 TGGAAACTCGGAGAGCTGCCCAAGGCAAGCTCGCCATCCCAAGTACTGTACAAGATCC 624
QY 860 ACTTATGCAAACTCTACTGTATCGCAGAGAATTGATTTCTTTCTTTGTCAATA 919
Db 625 ACAGAGCCCATGCTCTCGGGCCAGTAGAGTCTGTGACTC-----AAGG 672
QY 920 AAGTCAAGATGGGACTCCATGCTCGGAGGATAGCCGTAATGTTGTATAGTGGATAT 979
Db 673 ACATGGAGCTGGCACAATCAACCCCTGCACAGCAGGACCTTGGCTGGGACTGCCACAA 732
QY 980 GTGAGCTCAGTGTGTGTCCATCTGC--GCACATGCCCGACGCTCCCAAGAGAAGCCTC 1038
Db 733 AAGCAGCATTTCTGTGGAAGCGCAAGAAATACATGCCCGACGCTCCCAAGAGAAGCCTC 792
QY 1039 TTCACTTGGCAGATGAGTATAAGTCTTGTACGGCATAAAGGCTCTCTTGAAGTCC 1098
Db 793 TTCACTTGGCAGATGAGTATAAGTCTTGTACGGCATAAAGGCTCTCTTGAAGTCC 852
QY 1099 CATGAATATGAAGAACTGAACGTGAGAGACCTTGTGTGTGACAAAAAGATGATGCA 1158
Db 853 CATGAATATGAAGAACTGAACGTGAGAGACCTTGTGTGTGACAAAAAGATGATGCA 912
QY 1159 AACCATGGCCATGAATAATATACCACTAGCTGCTCAAGATACTCAACATGATCTGCT 1218
Db 913 AACCATGGCCATGAATAATATACCACTAGCTGCTCAAGATACTCAACATGATCTGCT 972
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QY	1219	TTATTCAAAGA-----	1229
Db	973	TTATTTCAAAGATGGAAACAATAGAGGAAAACATCAACATTGCAAATTGTAGTCTGATTCTT	1032
QY	1230	-----	1229
Db	1033	CTAGAAGATGAACAGCCAGGACTGGTGATTAAGTCAACCAGCAGACCACACCTTTAAGTAGC	1092
QY	1230	-----TGATTGATGGGGAAAGATGGGACTGCTCATGACCAAGCCATC	1272
Db	1093	TTCTGCCAGTGGCAGTCTGGATTGATGGGGAAAGATGGGACTGCTCATGACCAAGCCATC	1152
QY	1273	TTACTGACTGGTCTGGATATATGTTCTCTGGAAGATGAGCCCTGTGACACTTTGGGATT	1332
Db	1153	TTACTGACTGGTCTGGATATATGTTCTCTGGAAGATGAGCCCTGTGACACTTTGGGATT	1212
QY	1333	GCACCCATTAAGTGAATGTGTAAATATCGCAGCTGCACGAATTAATGAAGATACAGGT	1392
Db	1213	GCACCCATTAAGTGAATGTGTAAATATCGCAGCTGCACGAATTAATGAAGATACAGGT	1272
QY	1393	CTTGAGCTGGCCTTCAACCATTTGCCATGAGTCTGACACAACTTTGGCATGATCATGAT	1452
Db	1273	CTTGAGCTGGCCTTCAACCATTTGCCATGAGTCTGACACAACTTTGGCATGATCATGAT	1332
QY	1453	GGAGAAGGGAACTGTGTAAAAAGTCCGAGGGCAACATCATGTCCCTACATTTGGCAGGA	1512
Db	1333	GGAGAAGGGAACTGTGTAAAAAGTCCGAGGGCAACATCATGTCCCTACATTTGGCAGGA	1392
QY	1513	CGCAATGAGTCTTCTCCTGTGTCACCTTGACGCCGAGTATCTACACAAATTTCTAAGC	1572
Db	1393	CGCAATGAGTCTTCTCCTGTGTCACCTTGACGCCGAGTATCTACACAAATTTCTAAGC	1452
QY	1573	ACCGCTCAAGCTATCTGCTTGTGATCAGCCAAAGCCTGTGAAGGAATACAGTATCCT	1632
Db	1453	ACCGCTCAAGCTATCTGCTTGTGATCAGCCAAAGCCTGTGAAGGAATACAGTATCCT	1512
QY	1633	GAGAAATTGCCAGAGAAATTATATGATGCAAAACACACAGTGCAGTGGCAGTTCGAGAG	1692
Db	1513	GAGAAATTGCCAGAGAAATTATATGATGCAAAACACACAGTGCAGTGGCAGTTCGAGAG	1572
QY	1693	AAAGCCAAGCTGTGATGCTGGACTTTAAAAAGACATCTGTAAAGCCCTGTGTGCCAT	1752
Db	1573	AAAGCCAAGCTGTGATGCTGGACTTTAAAAAGACATCTGTAAAGCCCTGTGTGCCAT	1632
QY	1753	CGTATTGGAAGGAAATGTGAGACTAAATTTATGCCAGCAGAGAAAGGACAAATTTGTGGG	1812
Db	1633	CGTATTGGAAGGAAATGTGAGACTAAATTTATGCCAGCAGAGAAAGGACAAATTTGTGGG	1692
QY	1813	CATGACATGTGTGCCGGGAGGACAGTGTGTGAATATGTGATGAAGGCCCAAGCCC	1872
Db	1693	CATGACATGTGTGCCGGGAGGACAGTGTGTGAATATGTGATGAAGGCCCAAGCCC	1752
QY	1873	ACCCATGGCCACTGTGCGGACTGTCTTCTTGTGCCCATGCTCCAGAGCTGCGGAGGG	1932
Db	1753	ACCCATGGCCACTGTGCGGACTGTCTTCTTGTGCCCATGCTCCAGAGCTGCGGAGGG	1812
QY	1933	GGAGTATCTCATAGAGTGCCTCTGCACCAACCCCAAGCCATCGCATGGAGGGAAGTTTC	1992
Db	1813	GGAGTATCTCATAGAGTGCCTCTGCACCAACCCCAAGCCATCGCATGGAGGGAAGTTTC	1872
QY	1993	TGTGAGGCTCCACTCGCACTCTGAAGCTCTGCAACAGTCAAGAAATGTCCCGGGACAGT	2052
Db	1873	TGTGAGGCTCCACTCGCACTCTGAAGCTCTGCAACAGTCAAGAAATGTCCCGGGACAGT	1932
QY	2053	GTTGACTTCCGTGCTGCTCAGTGTGCCGAGCAACAAGCAGACGATTCAAGGGCGGCAC	2112
Db	1933	GTTGACTTCCGTGCTGCTCAGTGTGCCGAGCAACAAGCAGACGATTCAAGGGCGGCAC	1992
QY	2113	TACAAGTGAAGCCTTACACTCAAGTAGAAGATCAGGACTTATGCAAACTTACTGTATC	2172
Db	1993	TACAAGTGAAGCCTTACACTCAAGTAGAAGATCAGGACTTATGCAAACTTACTGTATC	2052
QY	2173	GCAGAAGGATTTGATTCTTCTTTCTTGTGTCAATAAAGTCAAAAGATGGGACTCCATGC	2232

Db	2053	GCAGAAGGATTTGATTCTTCTTCTTGTGTCAATAAAGTCAAAAGATGGGACTCCATGC	2112
QY	2233	TCGAGGATAGCCCGTAATGTTTGTATAGATGGGATATGTGAGAGAGTTGATGACAAT	2292
Db	2113	TCGAGGATAGCCCGTAATGTTTGTATAGATGGGATATGTGAGAGAGTTGATGACAAT	2172
QY	2293	GTCTTGATCTGATGCTGTGTGAAGACGTCTGTGGGGTGTGTACCGGGAATACTCAGCC	2352
Db	2173	GTCTTGATCTGATGCTGTGTGAAGACGTCTGTGGGGTGTGTACCGGGAATACTCAGCC	2232
QY	2353	TGCACGATTCAAGGGGTCTCTACACCAAGCACCACCAACCAACCACTATTATCACATG	2412
Db	2233	TGCACGATTCAAGGGGTCTCTACACCAAGCACCACCAACCAACCACTATTATCACATG	2292
QY	2413	GTCAACCATTCCTTCTGAGCCCGGAGTATCCGCATCTATGAATGAACGTCTCACTCC	2472
Db	2293	GTCAACCATTCCTTCTGAGCCCGGAGTATCCGCATCTATGAATGAACGTCTCACTCC	2352
QY	2473	TACATTTCTGTGCGCAATGCCCTCAGAAAGTACTACCTGAATGGGCACTGGAACCGTGAC	2532
Db	2353	TACATTTCTGTGCGCAATGCCCTCAGAAAGTACTACCTGAATGGGCACTGGAACCGTGAC	2412
QY	2533	TGGCCCCGCGGTACAAATTTTTCGGGCACTACTTTCGACTACAGACGGTCTTATATGAG	2592
Db	2413	TGGCCCCGCGGTACAAATTTTTCGGGCACTACTTTCGACTACAGACGGTCTTATATGAG	2472
QY	2593	CCCGAAGCTTAATCGCTACTGGAACCAACCAAGACACTGATTGTGAGCTGCTGTTT	2652
Db	2473	CCCGAAGCTTAATCGCTACTGGAACCAACCAAGACACTGATTGTGAGCTGCTGTTT	2532
QY	2653	CAGGGAAGGAACCCGGGTGTTCCTGGGAATACTCCATGCCCTCGCTTGGGAGCCGAGAG	2712
Db	2533	CAGGGAAGGAACCCGGGTGTTCCTGGGAATACTCCATGCCCTCGCTTGGGAGCCGAGAG	2592
QY	2713	CAGCCCCCTGCCAGCCCACTACACTTGGGCCATCGTGCCTCTGAGTGTCCGTGTCC	2772
Db	2593	CAGCCCCCTGCCAGCCCACTACACTTGGGCCATCGTGCCTCTGAGTGTCCGTGTCC	2652
QY	2773	TGCGAGGGGG 2783	
Db	2653	TGCGAGGGGG 2663	

RESULT 8			
US-10-217-774-5			
; Sequence 5, Application US/10217774			
; Publication No. US20020193583A1			
; GENERAL INFORMATION:			
; APPLICANT: Friddle, Carl Johan			
; APPLICANT: Hilbun, Erin			
; TITLE OF INVENTION: No. US20020193583A1e1 Human Proteases and Polynucleotides Encoding			
; TITLE OF INVENTION: Same			
; FILE REFERENCE: LEX-0219-USA			
; CURRENT APPLICATION NUMBER: US/10/217,774			
; CURRENT FILING DATE: 2002-08-12			
; PRIOR APPLICATION NUMBER: US/09/930,872			
; PRIOR FILING DATE: 2001-08-14			
; PRIOR APPLICATION NUMBER: US 60/225,852			
; PRIOR FILING DATE: 2000-08-16			
; NUMBER OF SEQ ID NOS: 5			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 5			
; LENGTH: 4042			
; TYPE: DNA			
; ORGANISM: homo sapiens			
US-10-217-774-5			
Query Match 64.8%; Score 1874.6; DB 13; Length 4042;			
Best Local Similarity 84.4%; Pred. No. 0;			
Matches 2287; Conservative 0; Mismatches 179; Indels 245; Gaps 6;			
QY	202	GCAGGACCTGCGTGCCTATGGAGCCCGCAGCGGACGGCCTGGAGCCCGAGCGTCC	261

Db 167 GCAGGCACCTGCGTGCGCCCATGAGGACCCGCGAGCGCAGCGCTGGGAGCCCGAGCGTCCC 226
Qy 262 GCGTCTCTCTCCACCCGCGAGCGGGCCGGGCTGGATGGAAGGGCGGGACATGGATGAA 321
Db 227 GCGTCTCTCTCCACCCGCGAGCGGGCCGGGCTGGATGGAAGGGCG----- 273
Qy 322 GCTGGAACCATCGTTCTCAGCAAACTAACAGAGAAACAGAAAACCAAACACTGCATGTT 381
Db 274 ----- 273
Qy 382 CTCACCTCAATAATGACCTGTGTCTGCTGACGAGTTGACACAGGGCGATTACGTGTCC 441
Db 274 -----AATATGACCTGTGTCTGCTGACGAGTTGACACAGGGCGATTACGTGTCC 326
Qy 442 CATGAATCATGCAACCATCAGCGCGGAGAAAGACAGTGGCCGTGTCGAGGTTGAGTCT 501
Db 327 CATGAATCATGCAACCATCAGCGCGGAGAAAGACAGTGGCCGTGTCGAGGTTGAGTCT 386
Qy 502 CTTCACTTCGCGCTGAAAAGCCCCAGCAGCACTTCCACATGATCTGAGACTTCCAGC 561
Db 387 CTTCACTTCGCGCTGAAAAGCGTCCAGGCAAGCTTCCACGTGATCTGAGACTTCCAGC 446
Qy 562 AGCCTAGTGGCTCCTGGCTTTATTTGTGACAGCTTGGAAAGACAGGCACTAAGTCTGTG 621
Db 447 AGCCTAGTGGCTCCTGGCTTTATTTGTGACAGCTTGGAAAGACAGGCACTAAGTCTGTG 506
Qy 622 CAGACTTTACCGCCAGAGACCTTCTGTTCTATCAAGGCTCTTGGATCACAAGAAAC 681
Db 507 CAGACTTTACCGCCAGAGACCTTCTGTTCTATCAAGGCTCTTGGATCACAAGAAAC 566
Qy 682 TCGGCATCGCATGAGGGAAGTTCTGTGAGGCTCCACTCGCACTGGAAGCTTGCAAC 741
Db 567 TCCTCA-----GTGGCCCTTCAACCTGCAAGGCTTGTCA 602
Qy 742 AGTCAGAAATGTCCTCCGCGGACAGTGTGACTTCCGTGCTGCATGTGCCGAGCACAAC 801
Db 603 GGCATGATACGAACAGAAAGGAGATTACTTCTTAAGGCACTTCTTCAACCTCTCA 662
Qy 802 AGCAGACGATTCAGAGGGCGGCACTACAAGTG--AAGCTTACACTCAAGTAGAAAGCCG 859
Db 663 TGGAAACTCGGAGAGCTGCCCAAGGAGCTGCCCATCCACGTACTGTACAAGAGATCC 722
Qy 860 ACTTATGCAAACTCTACTGTATCGCAGAAAGATTGATTTCTTTCTTTCTTGTCAATA 919
Db 723 ACAGAGCCCCCATGCTCTCGGGGCAAGTGAAGTCTGTGACCTC-----AAGG 770
Qy 920 AAGTCAAGATGGGACTCCATGCTCGAGAGATAGCCGTAATGTTGTATAGATGGATAT 979
Db 771 ACATGGAGGCTGACATCAACCCCTGCACAGAGCGAACCCTTGGGCTGGACGCCACAA 830
Qy 980 GTGAGCTCAGTGTGTGTCCACATCTGC-GCACATGCCCCAGCCTCCCAAGGAAGACCTC 1038
Db 831 AAGCAGCATTTCTGTGGAAGACGCAAGAAATACATGCCCCAGCCTCCCAAGGAAGACCTC 890
Qy 1039 TTTCATCTTGGCCAGATGAGTATAAGTCTTGCTTACGGCATTAAGGCTCTTTCTGAGGTC 1098
Db 891 TTTCATCTTGGCCAGATGAGTATAAGTCTTGCTTACGGCATTAAGGCTCTTTCTGAGGTC 950
Qy 1099 CATAGAAATGAAGAACTGAAAGTGGAGAACCTTGGTGTGTGTCGACAAAAAGATGACAA 1158
Db 951 CATAGAAATGAAGAACTGAAAGTGGAGAACCTTGGTGTGTGTCGACAAAAAGATGACAA 1010
Qy 1159 AACCATGGCCATGAAAAATATACCACTACGTGCTACGATACTCAACATGTGATCTGCT 1218
Db 1011 AACCATGGCCATGAAAAATATACCACTACGTGCTACGATACTCAACATGTGATCTGCT 1070
Qy 1219 TTATTCAAAGA----- 1229
Db 1071 TTATTCAAAGATGGAACAATAGAGGAACATCAACATTGCAATTGTAGGTCGATTCTT 1130
Qy 1230 ----- 1229

Db 1131 CTAGAAAGTGAACAGCCAGGACTGGTGAATAAGTCACACGCGAGACCAACCTTAAGTAGC 1190
Qy 1230 -----TGGAATTATGGGGAAGATGGAGCTCGTCATGACCAAGCCATC 1272
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Db 1251 TTAAGTCTGCTGTGAATATGTTCTTGGAAAGATGAGCCCTGTGACACTTGGGATTT 1310
Qy 1333 GCACCCATAGTGAATGTTGAATAATATCGAGCTGACGATTAATGAAGATACAGGT 1392
Db 1311 GCACCCATAGTGAATGTTGAATAATATCGAGCTGACGATTAATGAAGATACAGGT 1370
Qy 1393 CTTGACTGGCTTACCAATTGCCCATGAGTCTGACACAACTTTGGCATGATTCATGAT 1452
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Qy 1453 GGAGAAAGGAACATGTGTAAAAAGTCCGAGGGCAACATCATGTCCCTTACATTGGCAGGA 1512
Db 1431 GGAGAAAGGAACATGTGTAAAAAGTCCGAGGGCAACATCATGTCCCTTACATTGGCAGGA 1490
Qy 1513 CGCAATGAGTCTTCTCCTGTGTCACCTTGACGCCCGCAGTATCTACACAAATTTCTAAGC 1572
Db 1491 CGCAATGAGTCTTCTCCTGTGTCACCTTGACGCCCGCAGTATCTACACAAATTTCTAAGC 1550
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Qy 1693 AAAAGCAAGCTCTGCATGCTGGACTTTAAAAAGGACATCTGTAAAGCCCTGTGTCAT 1752
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Qy 1753 CGTATTGGAAGGAATGTGAGACTAAATTTATGCCAGCAGACAGAAAGGCACAAATTTGTGG 1812
Db 1731 CGTATTGGAAGGAATGTGAGACTAAATTTATGCCAGCAGACAGAAAGGCACAAATTTGTGG 1790
Qy 1813 CATGACATGTGTGCCCCGGGAGGACAGTGTGTGAATATGTGTGATGAAGGCCCAAGCCC 1872
Db 1791 CATGACATGTGTGCCCCGGGAGGACAGTGTGTGAATATGTGTGATGAAGGCCCAAGCCC 1850
Qy 1873 ACCCATGGCCACTGTGCGGACTGTCTTCTTGGTCCCCCATGCTCCAGGACCTGCGGAGGG 1932
Db 1851 ACCCATGGCCACTGTGCGGACTGTCTTCTTGGTCCCCCATGCTCCAGGACCTGCGGAGGG 1910
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Db 1911 GAGATATCATATGAGTGTGCTCTGCAACCAACCCCAAGCCATGCGATGAGGGAAGTTC 1970
Qy 1993 TGTGAGGCTTCACTCGCACTGTGAAGCTGTGCAACAGTCAGAAATGTCCCGGAGCAGT 2052
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Db 2031 GTTGACTTCGCTGCTCAGTGTGCGGAGCAACAAGCAGACGATTCAAGGGCGGAC 2090
Qy 2113 TACAAGTGAAGCCTTACACTCAAGTAGAAGATCAGAGCTTATGCAAACTTACTGTATC 2172
Db 2091 TACAAGTGAAGCCTTACACTCAAGTAGAAGATCAGAGCTTATGCAAACTTACTGTATC 2150
Qy 2173 GCAGAAAGATTGATTTCTTTCTTTGCAAAATAAAGTCAAAAGATGGGACTCCATGC 2232
Db 2151 GCAGAAAGATTGATTTCTTTCTTTGCAAAATAAAGTCAAAAGATGGGACTCCATGC 2210
Qy 2233 TCGAGAGATAGCCGTAATGTTGTATAGATGGATATGTGAGAGAGTGTGACAAAT 2292
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QY	2293	GTCTTGGATCTGATGCTGTGTAAGACGTCCTGTGGGGGTGTGTAA CGGGAATTA ACTAGCC	2352
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QY	2353	TGCACGATTCA GAGGGGTCTCTA CACCAAGCACCA CACACCAACCA GATTA TCACATG	2412
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QY	2413	GTCA CCAATTCCTTCTTGAGAGCCCGAGATATCCGCATCTATGAAATGAACGTCCTACCTCC	2472
Db	2391	GTCA CCAATTCCTTCTTGAGAGCCCGAGATATCCGCATCTATGAAATGAACGTCCTACCTCC	2450
QY	2473	TACATTTCTGTGCGCAATGCCCTCAGAAAGTA CTACCTGAATGGGCACTGGACCCGTGGAC	2532
Db	2451	TACATTTCTGTGCGCAATGCCCTCAGAAAGTA CTACCTGAATGGGCACTGGACCCGTGGAC	2510
QY	2533	TGGCCCGGCGGTACA AATTTTCGGGCACTACTTTCGACTACAGACGGTCTTATATGAG	2592
Db	2511	TGGCCCGGCGGTACA AATTTTCGGGCACTACTTTCGACTACAGACGGTCTTATATGAG	2570
QY	2593	CCCGAGAACTTAATCGCTACTGGA CCAACCAAGAGACA CTGATTTGTGAGCTGCTGTTT	2652
Db	2571	CCCGAGAACTTAATCGCTACTGGA CCAACCAAGAGACA CTGATTTGTGAGCTGCTGTTT	2630
QY	2653	CAGGGAAGGAACCCGGGTGTGCTTGGAATACTCCATGCGCTCGCTTGGGGACCGAGAAG	2712
Db	2631	CAGGGAAGGAACCCGGGTGTGCTTGGAATACTCCATGCGCTCGCTTGGGGACCGAGAAG	2690
QY	2713	CAGCCCCCTGCCCCAGCCAGACTACA CTTGGGCCATCGTGCGTCTGAGTGCTCCGTGTC	2772
Db	2691	CAGCCCCCTGCCCCAGCCAGACTACA CTTGGGCCATCGTGCGCTCTGAGTGCTCCGTGTC	2750
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RESULT 9
US-10-804-457-5
; Sequence 5, Application US/10804457
; Publication No. US20050065334A1
; GENERAL INFORMATION:
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Hilbun, Erin
; TITLE OF INVENTION: Novel Human Proteases and Polynucleotides Encoding the
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0219-USA
; CURRENT APPLICATION NUMBER: US/10/804,457
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US/10/217,774
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US/09/930,872
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,852
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4042
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-804-457-5

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Query Match	64.8%;	Score 1874.6;	DB 21;	Length 4042;
Best Local Similarity	84.4%;	Pred. No. 0;		
Matches 2287; Conservative	0;	Mismatches 179;	Indels 245;	Gaps 6;

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Db	167	GcAGGcAcCCTGcGtTgCGCCATgGgAcCCCGcAGCGGcGcCTTgGgAcCCCGAGcGCTCC	226
Oy	262	GcGTCTCTCTcAcCCCGGAGCGGcCGGcGTgATgGAAAGGcCGGcAcTgATgAA	321

Db	227	GGGCTCCTCCACCCGCGAGCGCGCGGCTGGATGGAAAAAGGGCG-----	273
QY	322	GCTGGAACCATCGTTCTGAGCAAACTAACACAGAAACAGAAAAACCAACACTGCATGTT	381
Db	274	-----	273
QY	382	CTCACTCAATATGACCTGGTCTCTGCTACGAGGTTGACCAACAGGGCGGATTAAGTGTCC	441
Db	274	-----AATATGACCTGGTCTCTGCTACGAGGTTGACCAACAGGGCGGATTAAGTGTCC	326
QY	442	CATGAATATGACCACTGACCGCGGAGAAAGACAGTGGCCGTGCCAGGTTGAGTCT	501
Db	327	CATGAATATGACCACTGACCGCGGAGAAAGACAGTGGCCGTGCCAGGTTGAGTCT	386
QY	502	CTTCACCTTCGGCTGAAAGGCCCCAGGCAAGACTTCCACATGATCTGAGACTTCCAGC	561
Db	387	CTTCACCTTCGGCTGAAAGGCCCCAGGCAAGACTTCCACATGATCTGAGACTTCCAGC	446
QY	562	AGCCTAGTGGCTCCTGGCTTATGTGACACGTTGGGAAAGACAGGCACTTAAGTCTGTG	621
Db	447	AGCCTAGTGGCTCCTGGCTTATGTGACACGTTGGGAAAGACAGGCACTTAAGTCTGTG	506
QY	622	CAGACTTTACCGCCAGAGGACTTCTGTTCTATCAAGGCTCTTGGATCACAGAAAC	681
Db	507	CAGACTTTACCGCCAGAGGACTTCTGTTCTATCAAGGCTCTTGGATCACAGAAAC	566
QY	682	TGCGCATCGCATGAGGGAAGTTCTGTAGGGCTCCACTCGCACTCTGAAGCTCTGCAAC	741
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QY	742	AGTCAGAAATGTCCCGGACAGTGTGACTTCCGTGCTCAGTGTGCCAGCACAAAC	801
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QY	802	AGCAGACGATTCAGAGGGCGGCACTACAAGTGG--AAGCCTTACACTCAAGTGAAGCCG	859
Db	663	TGGAACCTCGGCGAGAGCTGCCCAAGGACGCTGCCATCCACGTACTGTACAAGATCC	722
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QY	920	AAGTCAAGATGGGACTCCATGCTCGAGAGATAGCCGTAATGTTGTATAGATGGATAT	979
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Db	831	AAGCAGCATTTCTGTGGAAGACGCAAGAAATACATGCCCCAGCCTCCCAAGGAAGACCTC	890
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Db	891	TTCATCTTGGCCAGATGAGTATTAAGTCTTGCTTACGGCATTAAGCGCTCTTTCTGAGGTCC	950
QY	1099	CATAGAAATGAAGACTGAACCTGAGACCTTGTGTGTGTCGACAAAAGATGATGCAA	1158
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QY	1159	AACCATGGCCATGAAAAATATCACCACTACGCTGCTCAGCATACTCAACATGATCTGCT	1218
Db	1011	AACCATGGCCATGAAAAATATCACCACTACGCTGCTCAGCATACTCAACATGATCTGCT	1070
QY	1219	TTATTCAAAGA-----	1229
Db	1071	TTATTCAAAGATGGAACAATAGAGGAAACATCAACATTGCAATTGTAGGTCTGATTCTT	1130
QY	1230	-----	1229
Db	1131	CTAGAAGATGAACAGCCAGGACTGGTGAATAAGTCAACACGACAGACCACTTAAGTAGC	1190
QY	1230	-----TGATTGATGGGGAAGATGGGACTCGTCATGACCAAGCCATC	1272

Db 1191 TTCTGCCAGTGGCAGTCTGGAATTGATGGGAAGAATGGGACTGCTGTCATGACCAGCCATC 1250
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Db 1251 TTACTGACTGGTCTGGATATATGTTCTCTGGAAGATGAGCCCTGTGACACTTTGGGATTT 1310
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Qy 1393 CTTGGACTGGCCTTCAACCATTTGCCCATGAGTCTGGACACAACTTTGGCATGATTCATGAT 1452
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Db 1431 GGAGAAGGGAACATGTGTAAAGTCCGAGGGCAACATCATGTCCCCCTACATTGGCAGGA 1490
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Db 1851 ACCCATGGCCACTGGTCCGACTGGTCTTCTTGTGTCCTCCCATGCTCCAGGACCTGCGGAGGG 1910
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Db 1911 GGAGTATCTCATAGGAGTCCGCTCTGCACCAACCCCAAGCCATGCGATGAGGGAAGTTTC 1970
Qy 1993 TGTGAGGGCTCACTCGCACTCGAAGCTCTGCAACAGTCAGAAATGTCCCGGGAGCAGT 2052
Db 1971 TGTGAGGGCTCACTCGCACTCGAAGCTCTGCAACAGTCAGAAATGTCCCGGGAGCAGT 2030
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Qy 2173 GCAGAAGGATTTGATTTCTTTCTTTGTGCAATAAAGTCAAAAGATGGGACTCCATGC 2232
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Qy 2233 TCGAGAGATAGCCGTAATGTTGTATAGATGGATATGTGAGAGAGTTGGATGACAAT 2292
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Qy 2293 GTCTTGGATGATGCTGTGTAAGACGTCTGTGGGGTGTGTAAACGGAATACTCAGCC 2352
Db 2271 GTCTTGGATGATGCTGTGTAAGACGTCTGTGGGGTGTGTAAACGGAATACTCAGCC 2330

Qy 2353 TGCACGATTCAAGGGGTCTTCTACACCAAGACCAACCAACCAAGTATTAACATG 2412
Db 2331 TGCACGATTCAAGGGGTCTTCTACACCAAGACCAACCAACCAAGTATTAACATG 2390
Qy 2413 GTCAACATTCTTCTTGAGAGCCCGAGTATCCGATCTATGAATAATGAACGTCTTACCTCC 2472
Db 2391 GTCAACATTCTTCTTGAGAGCCCGAGTATCCGATCTATGAATAATGAACGTCTTACCTCC 2450
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Qy 2533 TGGCCCGCGGTACAAATTTTCGGGCACATACTTTCGACTACAGACGGTCTTATATGAG 2592
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Db 2691 CAGCCCTGCGCCAGCCCACTACACTTGCGCCATCGTGCCTGTAGTGTCTCCGTGCC 2750
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RESULT 10
US-09-981-151A-3
; Sequence 3, Application US/09981151A
; Publication No. US20030212256A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Gerlach, Valerie
; APPLICANT: Macdougall, John R
; APPLICANT: Malyankar, Muriel M
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A
; APPLICANT: Stone, David J
; APPLICANT: Gunther, Erik
; APPLICANT: Ellerman, Karen
; APPLICANT: Shinkets, Richard A
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Guo, Xiaojia
; APPLICANT: Patturajan, Meera
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Burgess, Catherine E
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Gangolli, Esha A
; APPLICANT: Fernandes, Elma R
; APPLICANT: Gorman, Linda
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-168
; CURRENT APPLICATION NUMBER: US/09/981,151A
; PRIOR APPLICATION NUMBER: 60/241,040
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,058
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,063
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,243
; PRIOR FILING DATE: 2000-10-17

; PRIOR APPLICATION NUMBER: 60/242,152
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/242,482
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,611
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,612
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,880
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/242,881
; PRIOR FILING DATE: 2000-10-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2433
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-981-151a-3

Query Match 62.0%; Score 1795.6; DB 10; Length 2433;
Best Local Similarity 82.0%; Pred. No. 0;
Matches 2375; Conservative 0; Mismatches 34; Indels 489; Gaps 7;

QY 1 CGCTCTGTGATGAAGCCCCCGCGCGGATGCGGGGCTTGGCGCGCTGTGATGCTG 60
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DB 82 CTGGCGCAGTGGCGCGAGCAGTGAAGTCCCGCGCGCTCCCAACGAGCGGAAACCGCGG 141
QY 121 TCCGGACAGTGGAGGCGAGTCCCCCGCGCTCTCTCCCGCGGACCCCGCGCTCTACC 180
DB 142 TCCGGACAGTGGAGGCGAGTCCCCCGCGCTCTCTCCCGCGGACCCCGCGCTCTACC 201
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DB 202 GCGATGTCCGCGCTGTTTTCGCAAGGACCTGCGGTGCGCATGGGACCCGCAAGCGGACG 261
QY 241 GCCTGGAGCGCCGAGCGTCCCGCGCTCTCTCTCAACCCGCGAGCGCGCGCTGATGGA 300
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DB 322 AAAGGCGCGACATGATGAAGCTGAAACCATGCTTCTCAAGCAAACTAACACAGGAACA 381
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DB 382 GAAACCAACAACCTGCATGTTCTCACTCCTGTAATATGACCTGGTCTCTGCTTACGAGTT 441
QY 418 GACCACAGGGGCGATTACGTGTCCCATGAATCATGACACCATCAAGCGGCGAGAAAGACA 477
DB 442 GACCACAGGGGCGATTACGTGTCCCATGAATCATGACACCATCAAGCGGCGAGAAAGACA 501
QY 478 GTGGCCGTGTCCGAGGTGAGTCTTTCACCTTCGGCTGAAAGGCCCGACGACTTC 537
DB 502 GTGGCCGTGTCCGAGGTGAGTCTTTCACCTTCGGCTGAAAGGCCCGACGACTTC 561
QY 538 CACATGATCTGAGGACTTTCAGACGACCTAAGTGGCTCCTGGCTTTATTGTGACAGCTTG 597
DB 562 CACATGATCTGAGGACTTTCAGACGACCTAAGTGGCTCCTGGCTTTATTGTGACAGCTTG 621
QY 598 GGAAGACAGGCACTAAGTCTGTGACAGACTTTAACCGCCAGAGGACTTCTGTTCTATCAA 657
DB 622 GGAAGACAGGCACTAAGTCTGTGACAGACTTTAACCGCCAGAGGACTTCTGTTCTATCAA 681
QY 658 GGCTCTTTGGATCACACAGAACTCGCCATCGCATGAGGGAAGTTCTGTAGGGCTCC 717
DB 682 GGCTCTTTGGATCACACAGAACTCCCCATCGCATGAGGGAAGTTCTGTGAGGGCTCC 741

QY 718 ACTGCACTCTGAAGCTCTGCAACAGTGAAGAAATGTCCCGGAGACAGTGTGACTTCCGT 777
DB 742 ACTGCACTCTGAAGCTCTGCAACAGTGAAGAAATGTCCCGGAGACAGTGTGACTTCCGT 801
QY 778 GCTGCTCAGTGTGCCGAGCAACAACAGACAGCATTCAGAGGGCGGCACTCAAGTGGAG 837
DB 802 GCTGCTCAGTGTGCCGAGCAACAACAGACAGCATTCAGAGGGCGGCACTCAAGTGGAG 861
QY 838 CCTTACACTCAAGTAGAAGCCGACTTTATGCAAACTCTACTGTATCGCAAGAGATTGAT 897
DB 862 CCTTACACTCAAGTAGAAGCCGACTTTATGCAAACTCTACTGTATCGCAAGAGATTGAT 921
QY 898 TTCTTCTTTCTTTGTCAAAATAAAGTCAAAAGATGGACTCCATGCTCGAGAGATAGCCGT 957
DB 922 TTCTTCTTTCTTTGTCAAAATAAAGTCAAAAGATGGACTCCATGCTCGAGAGATAGCCGT 981
QY 958 AATGTTGTATAGATGGATATGTGAGCTCAGTGTGTCCACATCTGCGCACATGCC 1017
DB 982 AATGTTGTATAGATGGATATGTGAG-----ATGCC 1014
QY 1018 CAGCCTCCCAAGAAAGACTCTTCATCTTGCCAGATGATATAAGTCTTGCTTACGGCAT 1077
DB 1015 CAGCCTCCCAAGAAAGACTCTTCATCTTGCCAGATGATATAAGTCTTGCTTACGGCAT 1074
QY 1078 AAGCGTCTCTTCTGAGGTCCCATAGAAATGAAGAACTGAACGTGAGACCTTGTGTTG 1137
DB 1075 AAGCGTCTCTTCTGAGGTCCCATAGAAATGAAGAACTGAACGTGAGACCTTGTGTTG 1134
QY 1138 GTGACAAAAGATGATGCAAAAACCATGGCCATGAATAATCACCACTACGTGCTCAG 1197
DB 1135 GTGACAAAAGATGATGCAAAAACCATGGCCATGAATAATCACCACTACGTGCTCAG 1194
QY 1198 ATACTCAACATGATGATCTGCTTATTCAAAGATGATGATGGGAAAGATGGACTGCT 1257
DB 1195 ATACTCAACATGATGATCTGCTTATTCAAAGATGATGATGGGAAAGATGGACTGCT 1238
QY 1258 CATGACCAAGCCATCTTACTGACTGCTGATATATGTTCTGGAAGATGAGCCCTGT 1317
DB 1239 ----- 1238
QY 1318 GACACTTTGGATTGCAACCATAGTGAATGTGTAGTAAATATCGACGTGACAGATT 1377
DB 1239 -----AGAAAACATCAACATTGCAATTGT 1262
QY 1378 AATGAAGTACAGGTCTTGGACTGGCTTCACCATTGCCCATGAGTCTGGAACAACCTTT 1437
DB 1263 AGTCTGATT----- 1273
QY 1438 GGCATGATTCATGATGAGAAGGAACATGTGTAAAAAGTCCGAGGCAACATCATGTCC 1497
DB 1274 ----- 1273
QY 1498 CTTACATTGGCAGACGCAATGAGTCTTCTCTGTGTCAACCTGACGCCAGATATCTA 1557
DB 1274 ----- 1273
QY 1558 CACAATTCTAAGCACCGCTCAAGCTATCTGCCCTGTGATCAGCCAAAGCCTGTGAAG 1617
DB 1274 ----- 1273
QY 1618 GAATACAGTATCCTGAGAAATTGCCAGAGAAATTATGATGCAAAACACAGTGCAAG 1677
DB 1274 ----- 1273
QY 1678 TGCGAGTTCGAGAGAAAGCCAGCTCTGCATGCTGGACTTTAAAAAGACATCTGTAAA 1737
DB 1274 -----TTCTAGAAAGATGAACGAGACATCTGTAAA 1302
QY 1738 GCCCTGTGTGCCATCTGATTGGAAGAAATGTGAGACTAAATTTATGCCAGACAGCAAA 1797
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Db      1363 GGCACAATTGTGGGCATGACATGTGTGCCGGGAGAGACAGTGTGTGAATATGGTGAT 1422
QY      1858 GAAGGCCCCCAAGCCCCCAATGAGCCACTGGTCGAGACTGGTCTTCTTGGTCCCATGCTCC 1917
Db      1423 GAAGGCCCCCAAGCCCCCAATGAGCCACTGGTCGAGACTGGTCTTCTTGGTCCCATGCTCC 1482
QY      1918 AGGACCTGCGGAGGGGAGATATCTCATAGAGTGCCTCTGCAACCAACCCCAAGCCATCG 1977
Db      1483 AGGACCTGCGGAGGGGAGATATCTCATAGAGTGCCTCTGCAACCAACCCCAAGCCATCG 1542
QY      1978 CATGAGGGGAAGTTCTGTGAGGGGCTCCACTCGCACTCTGAAGCTCTGCAACAGTCAGAAA 2037
Db      1543 CATGAGGGGAAGTTCTGTGAGGGGCTCCACTCGCACTCTGAAGCTCTGCAACAGTCAGAAA 1602
QY      2038 TGTCCCCGGGACAGTGTGACTTCCGTGCTGCTCAGTGTGCCGAGCAACAAGCAGACGA 2097
Db      1603 TGTCCCCGGGACAGTGTGACTTCCGTGCTGCTCAGTGTGCCGAGCAACAAGCAGACGA 1662
QY      2098 TTCAGAGGGCGGCACTACAAGTGGAAAGCCTTACACTCAAGTAGAAGATCAGACTTATGC 2157
Db      1663 TTCAGAGGGCGGCACTACAAGTGGAAAGC-----TCAGACTTATGC 1704
QY      2158 AAACCTCTACTGTATCGCAGAAAGATTGATTTCTTTCTTGTCAATAAAGTCAAA 2217
Db      1705 AAACCTCTACTGTATCGCAGAAAGATTGATTTCTTTCTTGTCAATAAAGTCAAA 1764
QY      2218 GATGGAGCTCCATGCTCGAGAGATAGCCGTAATGTTGTATAGATGGGATATGAGAGA 2277
Db      1765 GATGGAGCTCCATGCTCGAGAGATAGCCGTAATGTTGTATAGATGGGATATGAGAG--- 1821
QY      2278 GTTGGATGTGACATGTCTCTGGATCTGATGCTGTGAAGACGTGTGGGGTGTGAAC 2337
Db      1822 ---GGATGTGACATGTCTCTGGATCTGATGCTGTGAAGACGTGTGGGGTGTGAAC 1878
QY      2338 GGGATACTAGCTGAGCTGACAGATTACAGGGGTCTTACACCAAGCACCAACCAAC 2397
Db      1879 GGGATACTAGCTGAGCTGACAGATTACAGGGGTCTTACACCAAGCACCAACCAAC 1938
QY      2398 CAGTATTATCACATGTGTCACCATCTCTTGTGAGCCCGAGATATCCGCATCTATGAATG 2457
Db      1939 ---TATTATCACATGTGTCACCATCTCTTGTGAGCCCGAGATATCCGCATCTATGAATG 1995
QY      2458 AACGTCTTACCTCCTACATTTCTGTGCGCAATGCCCTCAGAAAGTACTACTGAATGG 2517
Db      1996 AACGTCTTACCTCCTACATTTCTGTGCGCAATGCCCTCAGAAAGTACTACTGAATGG 2055
QY      2518 CACTGGAACCGTGAAGTGGCCCGGCTACAATTTTCGGGCACTACTTTCGACTACAGA 2577
Db      2056 CACTGGAACCGTGAAGTGGCCCGGCTACAATTTTCGGGCACTACTTTCGACTACAGA 2115
QY      2578 CGGTCTTATAATGAGCCCGGAGAACTTAATCGCTACTGACCAACCAAGAGACACTGATT 2637
Db      2116 CGGTCTTATAATGAGCCCGGAGAACTTAATCGCTACTGACCAACCAAGAGACACTGATT 2175
QY      2638 GTGAGCTGCTGTTTTCAGGGAAGAACCCGGGTGTGCTGGGAATACTCCATGCTCGC 2697
Db      2176 GTGAGCTGCTGTTTTCAGGGAAGAACCCGGGTGTGCTGGGAATACTCCATGCTCGC 2235
QY      2698 TTGGGGACCGGAGAACAGAGCCCTGCCCCAGCCCACTACACTTGGGCCATCGTGGCTCT 2757
Db      2236 TTGGGGACCGGAGAACAGAGCCCTGCCCCAGCCCACTACACTTGGGCCATCGTGGCTCT 2295
QY      2758 GAGTGTCTCCGTGCTTCCGAGAGGGGGTAGTGTGCTTCCAGTGTGCTCTCTGAGGACGA 2817
Db      2296 GAGTGTCTCCGTGCTTCCGAGAGGGGGTAGTGTGCTTCCAGTGTGCTCTCTGAGGACGA 2355
QY      2818 TGTCAAGCTTTCAGGCACTGCGTACATTGCACTGGCCTTCTTGAATCCTAATGACAGCC 2877
Db      2356 TGTCAAGCTTTCAGGCACTGCGTACATTGCACTGGCCTTCTTGAATCCTAATGACAGCC 2415
QY      2878 CGGGGCTTCTCCTGCCA 2895
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Db      2416 CGGGGCTTCTCCTGCCA 2433

RESULT 11
US-09-981-151A-5
; Sequence 5, Application US/09981151A
; Publication No. US20030212256A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Gerlach, Valerie
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Muriel M
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A
; APPLICANT: Stone, David J
; APPLICANT: Gunther, Erik
; APPLICANT: Ellerman, Karen
; APPLICANT: Shimkets, Richard A
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Guo, Xiaojia
; APPLICANT: Patlurajan, Meera
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Burgess, Catherine E
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Gangolli, Esha A
; APPLICANT: Fernandes, Elma R
; APPLICANT: Gorman, Linda
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-168
; CURRENT APPLICATION NUMBER: US/09/981,151A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 60/241,040
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,058
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,063
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,243
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/242,152
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/242,482
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,611
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,612
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,880
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/242,881
; PRIOR FILING DATE: 2000-10-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 2902
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-981-151A-5

Query Match      58.5%; Score 1695; DB 10; Length 2902;
Best Local Similarity 78.1%; Pred. No. 0;
Matches 2333; Conservative 0; Mismatches 315; Indels 339; Gaps 11;

QY      40 TTGGCGCGCTGTGATGCTGTGGCGCAGGTGGCCGAGCAGTGAATCCCGGGCGCTCC 99
Db      1 TTGGCGCGCTGTGATGCTGTGGCGCAGGTGGCCGAGCAGTGAATCCCGGGCGCTCC 60
QY      100 CACCAGCGCGAAACCGGGTCCGGACAGCTGAGAGGCGGAGTCCCCCGGCTCTCTCC 159
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Db 61 CACCAGCGCGGAAACCGCGGTCGGACAGCTGGAGGCGAGTCCCCGCGGCTCCTCTCC 120
 QY 160 CGCGGACCCCGCGCTCTACCCGGATGTGCGCGCTGTTTCCGACAGGCACTGCGTGGC 219
 Db 121 CGCGGACCCCGCGCTCTACCCGGATGTGCGCGCTGTTTCCGACAGGCACTGCGTGGC 180
 QY 220 CATGGACCCCGCAGCGGCGAGCGCTGGAGCCGAGCGCTCCGCGCTCTCTCCACCCGC 279
 Db 181 CATGGACCCCGCAGCGGCGAGCGCTGGAGCCGAGCGCTCCGCGCTCTCTCCA----- 235
 QY 280 GGAGCGGCGCGGCTGGATGAAAAAGGCGGGAATGATGAAGCTGMAACCATCGTTCT 339
 Db 236 ----- 235
 QY 340 CAGCAAACTAACA CAGMAACGMAAAACCAACA CTGATGTTCTCACTCAATATGACCTG 399
 Db 236 -----GACCTG 241
 QY 400 GTCTCTGCTACGAGGTTGACCA CAGGGCGAATTACGTGCCATGAATCATGCAACCAT 459
 Db 242 GTCTCTGCTACGAGGTTGACCA CAGGGCGAATTACGTGCCATGAATCATGCAACCAT 301
 QY 460 CAGCGGCGGAGAGAGAGAGAGTGGCGGTGTCGAGGTTGAGTCTTCACTTGGGCTGAAA 519
 Db 302 CAGCGGCGGAGAGAGAGAGAGTGGCGGTGTCGAGGTTGAGCCAGCTTCTCCAGGTATGC 361
 QY 520 GGGCCGAGGCAAGCTTCCACATGATCTGAGGACTTCCAGCAGCTAGTGGCTCTGGC 579
 Db 362 AGAGCCAGAGAGCTCAGACT-----GTGTGAGAGGCTTTCCATTGCTAATCTCAGC 416
 QY 580 TTTATGTGACAGCGTTGGGAAAGACAGGCACTAAGTCTGTGACACTTTA CCGCAGAG 639
 Db 417 CGGGGTTTGAACCTTTCATGTTCGTCTCACTGAGGGAACAGCATGCTTCCAGA 476
 QY 640 GACTTCTGTTCTATCAAGGCTTTGCGATCACACAGAACTCGCCATCGCATGGAGG 699
 Db 477 GAATAATAACAATGCAA-----TGCTTGAGAAATCGGCCCTGGCTTCAACAGAAAG 529
 QY 700 AAGTTCTGTAGGGCTCCACTGCACTGTGAAGCTCTGCAACAGTCAGAAATGTCCCGG 759
 Db 530 TCTAATGTGTTTCTTCTTCTTCTTATTTTTCAGTCAAGGCATGATAGAAAGAA 589
 QY 760 GACAGTGTGACTTCCGTGTGCTCAGTGTGCCAGACACAGACAGATTCAGAGG 819
 Db 590 GAGGCAAGTATCTTCTTAAGGCACTTCTTCAACCTCTCATGGAACCTCGGCAAGCT 649
 QY 820 CGGCACTACAAGTG--AAGCTTACACTCAAGTAGAAGCCGACTTATGCAACTCTACT 877
 Db 650 GCCCAAGGAGCTCGCCATCCCACTGTAACAAGAGAGGTCTGTGACTCAAGG 709
 QY 878 GTATGACAGAGGATTTGATTTCTTCTTGTCAATAAAGTCAAGATGGGACTC 937
 Db 710 ACATGGAGC-----TGGCACAATCAACCCCTGCA CAGCAGCGA 747
 QY 938 CATGCTCGAGGATAGCCGTAATGTTGATAGATGGATATGTAGCTCAGTGTGT 997
 Db 748 CCTTCGCTGGAGCTGCCAAGAGAGCAATTTCTGTGAAGACGCAAGAAAT----- 800
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 Db 801 -----ACATGCCAGCCTCCCAAGGAAGACCTTTCTATCTTGCAGATGAGT 848
 QY 1058 ATAAGTCTTGCTTACGSCATAGCGCTCTTCTGAGGTCCCATAGAAATGAAGAACTGA 1117
 Db 849 ATAAGTCTTGCTTACGSCATAGCGCTCTTCTGAGGTCCCATAGAAATGAAGAACTGA 908
 QY 1118 ACGTGAGACCTTGTGTGTGTCGACAAAAGATGATGCAAAAACCATGGCCATGAAATA 1177
 Db 909 ACGTGAGACCTTGTGTGTGTCGACAAAAGATGATGCAAAAACCATGGCCATGAAATA 968
 QY 1178 TCACCACTAAGTGTCTACAGATACTCAACATGGTATCTGCTTATTCAAGA----- 1229
 Db 969 TCACCACTAAGTGTCTACAGATACTCAACATGGTATCTGCTTATTCAAGATGGAACAA 1028

QY 1230 ----- 1229
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 Db 1089 GACTGTGATTAAGTACCA CGCAGACCA CACCTTAAGTATTTCTGCCAGTGGCAGTCTG 1148
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 QY 1292 TATGTTCTGGAAGATGAGCCCTGTGACACTTTGGGATTTGCA CCCCATTAAGTGAATGT 1351
 Db 1209 TATGTTCTGGAAGATGAGCCCTGTGACACTTTGGGATTTGCA CCCCATTAAGTGAATGT 1268
 QY 1352 GTAGTAAATATCGCAGCTGCAAGATTATGAAGATACAGGCTTGAGCTGGCCTTGACCA 1411
 Db 1269 GTAGTAAATATCGCAGCTGCAAGATTATGAAGATACAGGCTTGAGCTGGCCTTGACCA 1328
 QY 1412 TTGCCATGAGTCTGGACACA CACTTTGGCATGATTCAATGATGAGAGGGAACATGTGTA 1471
 Db 1329 TTGCCATGAGTCTGGACACA CACTTTGGCATGATTCAATGATGAGAGGGAACATGTGCA 1388
 QY 1472 AAAAGTCCGAGGGCAACATCATGTGCCCTTACATTGGGAGGACGCAATGAGTCTTCTCT 1531
 Db 1389 AAAAGTCCGAGGGCAACATCATGTGCCCTTACATTGGGAGGACGCAATGAGTCTTCTCT 1448
 QY 1532 GGTACCCCTGACGCGCGCATATCTACACA AATTTCTAAGCACCGCTCAAGCTATCTGCC 1591
 Db 1449 GGTACCCCTGACGCGCGCATATCTACACA AATTTCTAAGCACCGCTCAAGCTATCTGCC 1508
 QY 1592 TTGCTGATCAGCCAAAGCCTGTGAAGGATACAAAGTATCTGAGAAATTGCCAGAGAAAT 1651
 Db 1509 TTGCTGATCAGCCAAAGCCTGTGAAGGATACAAAGTATCTGAGAAATTGCCAGAGAAAT 1568
 QY 1652 TATATGATGCAAAACACACAGTGCAGTGGCAGTTCCGAGAGAAAGCCAAAGCTCTGCATGC 1711
 Db 1569 TATATGATGCAAAACACACAGTGCAGTGGCAGTTCCGAGAGAAAGCCAAAGCTCTGCATGC 1628
 QY 1712 TGGACTTTAAAAAGACATCTGTAAAGCCCTGTGTGCCATCGTATTTGAAAGAAATGTG 1771
 Db 1629 TGGACTTTAAAAAGACATCTGTAAAGCCCTGTGTGCCATCGTATTTGAAAGAAATGTG 1688
 QY 1772 AGACTTAATTTATGCCAGCAGCAGAAAGCCAAATTTGTGGCATGACATGTGTGCCGG 1831
 Db 1689 AGACTTAATTTATGCCAGCAGCAGAAAGCCAAATTTGTGGCATGAAATGTGTGCC--G 1745
 QY 1832 GAGGACGTGTGTGAATATGTGTGAAGGGCCCCAAGCCCACTGAGGCCACTGTGTGG 1891
 Db 1746 GAGGACGTGTGTGAATATGTGTGAAGGGCCCCAAGCCCACTGAGGCCACTGTGTGG 1805
 QY 1892 ACTGCTTCTTGTGCCCATGTGTCAGGACCTGCGAGGGGGAGTA TCTATAGAGTCTC 1951
 Db 1806 ACTGCTTCTTGTGCCCATGTGTCAGGACCTGCGAGGGGGAGTA TCTATAGAGTCTC 1865
 QY 1952 GC---CTCTGACCAAACCCCAAGCCATGCGATGAGGGAAGTTCTGTGAGGGCTCCACTC 2008
 Db 1866 GCTCTCAAAATACACTTCAGAGCCATGCGATGAGGGAAGTTCTGTGAGGGCTCCACTC 1925
 QY 2009 GCACTTGAAGCTCTGCAACAGTCAAGAAATGTCCCGGGAACAGTGTGA CTTCGCTG 2068
 Db 1926 GCACTTGAAGCTCTGCAACAGTCAAGAAATGTCCCGGGAACAGTGTGA CTTCGCTG 1985
 QY 2069 CTCAAGTGCAGGACCAACAGCAGATTCAGAGGGCGGCACTACAGTGAAGCTT 2128
 Db 1986 CTCAAGTGCAGGACCAACAGCAGATTCAGAGGGCGGCACTACAGTGAAGCTT- 2044
 QY 2129 ACACTCAAGTAGAAGTCAAGACTTATGCAAACTTA CTGTATCGCAGAAAGATTTGATT 2188
 Db 2045 -----GATCAGGACTTATGCAAACTTA CTGTATCGCAGAAAGATTTGATT 2090


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Db      1403 GCAACATCATGTCCCCCTACATGTGGCAGGACGCAATGAGTCTTCTCCTGTGCAACCCTGCA 1462
Qy      1544 GCCGCCAGTATCTACACAATTTCTAAGCACCGCTCAAGCTATCTGCTTGCTGATCAGC 1603
Db      1463 GCCGCCAGTATCTACACAATTTCTAAGCACCGCTCAAGCTATCTGCTTGCTGATCAGC 1522
Qy      1604 CAAAGCCTGTGAAGGAATACAAATCTCTGAGAAATGGCCAGAGAAATTAATGATGCAA 1663
Db      1523 CAAAGCCTGTGAAGGAATACAAATCTCTGAGAAATGGCCAGAGAAATTAATGATGCAA 1582
Qy      1664 ACACACAGTGCAGAGTGGCAGTTCGAGAGAGAAAGCCAAAGCTTGCACTGCTGGACTTTAAA 1723
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Db      1643 AGGACATCTGTAAAGCCCTGTGGTGCATCGTATTTGAAGGAAATGTGAGACTAAATTTA 1702
Qy      1784 TGCCAGCAGCAGAGGACACAATTTGTGGGCAATGACATGTGTGCCGGGAGACAGTGTG 1843
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Qy      1844 TGAATATATGTGATGAAGGCCCAAGCCCAATGAGGCACTGCTGAGCTGCTTCTT 1903
Db      1763 TGAATATATGTGATGAAGGCCCAAGCCCAATGAGGCACTGCTGAGCTGCTTCTT 1822
Qy      1904 GGTCCCCATGCTCCAGGACCTGCGGAGGGGAGATATCTCATAGAGAGTCCGCTCTGCACCA 1963
Db      1823 GGTCCCCATGCTCCAGGACCTGCGGAGGGGAGATATCTCATAGAGAGTCCGCTCTGCACCA 1882
Qy      1964 ACCCCCAAGCCATCGCATGAGAGGAAGTCTGTGAGGGGCTCCACTCGCACTCTGAAGCTCT 2023
Db      1883 ACCCCCAAGCCATCGCATGAGAGGAAGTCTGTGAGGGGCTCCACTCGCACTCTGAAGCTCT 1942
Qy      2024 GCAACAGTCAGAAATGTCCCCCGGACAGTGTGACTTCCGTGCTGCTCAAGTGTCCGAGC 2083
Db      1943 GCAACAGTCAGAAATGTCCCCCGGACAGTGTGACTTCCGTGCTGCTCAAGTGTCCGAGC 2002
Qy      2084 ACAACAGCAGACGATTCAGAGGGCGGCACTACAGTGAAGCCTTACACTCAAGTAGAAG 2143
Db      2003 ACAACAGCAGACGATTCAGAGGGCGGCACTACAGTGAAGCCTTACACTCAAGTAGAAG 2062
Qy      2144 ATCAGGACTTATGCAAACTCTACTGTATCGCAGAAAGATTCTTCTTCTTCTTGT 2203
Db      2063 ATCAGGACTTATGCAAACTCTACTGTATCGCAGAAAGATTCTTCTTCTTCTTGT 2122
Qy      2204 CAAATAAAGTCAAAGATGGGACTCCATGCTCGGAGGATAGCCGTAATGTTGTATAGATG 2263
Db      2123 CAAATAAAGTCAAAGATGGGACTCCATGCTCGGAGGATAGCCGTAATGTTGTATAGATG 2182
Qy      2264 GGATATGTGAGAGAGTGGATGTGCAATGTCTTGGATCTGATGCTGTGTAAGACGTCT 2323
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Qy      2324 GTGGGGTGTGTAACGGGAATTACTAGCCTGCAAGATTCAAGGGGTCTCTACACCAAGC 2383
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Qy      2384 ACCACCAACCAACCAAGTATTAATCAATGTGTCACCAATTCCTTCTGAGCCCGGAGTATCC 2443
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Qy      2444 GCATCTATGAAATGAACGTCTCTACTCTCTCAATTTCTGTGGCAATGCCCTCAGAAAGGT 2503
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Db      2423 ACTACCTGAATGGGCACTGGAACCGTGACTGGCCCGGCGGCTCAAAATTTTGGGCACTA 2482
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Db      2543 ACAGACACTGATTTGTGAGCTGCTGTTTCAGGGAAGAAACCGGGTGTGCTGGGAAT 2602
Qy      2684 ACTCATGCTCTGCTTGGGGACCGAGACGACCCCTGCCAGCCCACTACACTTGGG 2743
Db      2603 ACTCATGCTCTGCTTGGGGACCGAGACGACCCCTGCCAGCCCACTACACTTGGG 2662
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Db      2663 CCATGTCGCTCTGAGTGTCTCCGTGCTCGGAGGGGG 2702
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RESULT 13

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US-10-363-937-34
; Sequence 34, Application US/10363937
; Publication No. US20040053269A1
; GENERAL INFORMATION:
; APPLICANT: Todd, Stephen; Delegeane, Angelo M.;
; APPLICANT: Gandhi, Ameena R.; Nguyen, Daniel B.;
; APPLICANT: Hafalla, April J.A.; Kearney, Liam;
; APPLICANT: Lu, Yan; Lee, Ernestine A.;
; APPLICANT: Chawla, Narinder K.; Das, Debopriya;
; APPLICANT: Arvizu, Chandra S.; Yao, Monique G.;
; APPLICANT: Kallick, Deborah A.; Elliott, Vicki S.;
; APPLICANT: Ding, Li; Yue, Henry;
; APPLICANT: Reddy, Roopa; Burford, Neil;
; APPLICANT: Baughn, Mariah R.; Lal, Preeti G.;
; APPLICANT: Borowsky, Mark L.; Lu, Dyrung Aina M.;
; APPLICANT: Ramkumar, Jayalaxmi; Yang, Junming;
; APPLICANT: Tribouley, Catherine M.; Khan, Farrah A.;
; APPLICANT: Gururajan, Rajagopal; Tang, Y. Tom;
; APPLICANT: Au-Young, Janice; Warren, Bridget A.;
; APPLICANT: Hernandez, Roberto; Duggan, Brendan M.
; TITLE OF INVENTION: PROTEASES
; FILE REFERENCE: PI-0212 USN
; CURRENT APPLICATION NUMBER: US/10/363, 937
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: PCT/US01/28161
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: US 60/231, 039
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US 60/232, 812
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/234, 850
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/236, 500
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/238, 773
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 60/239, 658
; PRIOR FILING DATE: 2000-10-11
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PERL Program
; SEQ ID NO 34
; LENGTH: 3389
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040053269A1 7478405CB1
US-10-363-937-34
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Query Match      24.5%; Score 709.6; DB 18; Length 3389;
Best Local Similarity 65.0%; Pred. No. 1.2e-212;
Matches 1081; Conservative 0; Mismatches 579; Indels 4; Gaps 2;
Qy      1124 AGACCTGTGTGTGTCACAAAAGATGATGCAAAACCATGAGCCATGAAAATATACCA 1183
Db      1096 AAACGTGTGTGTGAGCCTAATTCCTCTGGAACAAGAACCTGAGGATTATTGATCAA 1155
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QY 1184 CCTACGTGCTCAGCACTACTCAACATGGTATCTGCTTTATTCAAGATGGATTGATGGGA 1243
Db 1156 CCATCATGACAGACAGTCTCTGAATAGTTTTTG--TCAATGAGAGTCTGCCCTCATTTGGAA 1214
QY 1244 AAGATGGAGCTGCTATGACAGCCCATCTTACTGACTGTCTGATATATATGTTCTTGA 1303
Db 1215 AGAATGGCAAGACATGATCATGCTCATTAAGATTTGATATTTGTTCTTGA 1274
QY 1304 AGAATGAGCCCTGTGACACTTTGGGATTTGACCCATTAAGTGAATGTAGTAAATATC 1363
Db 1275 AGAATGAACCATGTGACACTTAGGGTTTGCCCATCAGTGAATGTGCTCTAAGTACC 1334
QY 1364 GCAGCTGACAGATTATGAAGATACAGGTCTTGAAGCTGCTTCAACCATTTGCCATGAGT 1423
Db 1335 GAAGTTGTACCATCATGAGACACAGGACTTGGCCTTGCTTCAACCATCGCTCATGAGT 1394
QY 1424 CTGACACAACTTTGGCATGATTCATGATGAGAAAGGAACATGTTAAAGTCCGAGG 1483
Db 1395 CAGGGCACAACCTTTGGTATGATTCACGACGAGAAAGGAATCCCTGCAGAAAGGCTGAG 1454
QY 1484 GCAACATCATGTCCCTTACATTTGGCAGGACGCAATGGAAGTCTTCTCTGCTCACCCCTGA 1543
Db 1455 GCAATATCATGTCTCCACACCTGACCGGAAACAATGGAAGTGTTCATGTCTTCTCTGCA 1514
QY 1544 GCCGCCAGTATCTACAAATTTCTAAGCACCGCTCAAGCTATCTGCTTGCCTGATCAGC 1603
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QY 1604 CAAAGCCTGTGAAGAAATCAAGATATCCTGAGAAATTTGCCAGAGAAATTAATGATGCAA 1663
Db 1575 CCAAGCAAGCAGACAGTATTAATATCCGGACAAATACTACAGACAGATTTATGATGCTG 1634
QY 1664 ACACACAGTGCAGAGTGGCAGTTCCGAGAGAGAAAGCCAAAGCTCTGCACTGACTTTAAA 1723
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QY 1724 AGGACATCTGTAAAGCCCTGTGTGCCATCGTATTTGGAAGAAATGTGAGACTTAATTTA 1783
Db 1695 AGGATATTTGCAAAATCACTTTGTGTGCCACCGAGTAGGCCACAGGTGTGAGACCAAGTTTA 1754
QY 1784 TGCCAGCAGCAGAAAGCACAATTTGTGGCATGACATGTGTGCGGGGAGAGACAGTGTG 1843
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Db 1815 TAAAGTTGGGAGCTCGGGCCCCCGCCATCCAGGCCAGTGTGCGCTGTGCAAGT 1874
QY 1904 GGTCCCCATGCTCCAGGACCTCGGAGGGGAGGTATCTCATAGAGAGTGGCTCTGCACCA 1963
Db 1875 GGTCAGAATGTTCCGGACATGTGTGAGAGAGTCAAGTTCAGAGAGACACTGCAATA 1934
QY 1964 ACCCCAAAGCCATCGCATGGAGGAAAGTCTGTGAGGGCTCCACTCGCACTCTGAAGCTCT 2023
Db 1935 ACCCCAAAGCCTCAGTATGTGTGATATTCTGTCAAGGTTCTAGCCGTATTATCAGCTGT 1994
QY 2024 GCACACAGTCAAGAAATGTCCCGGGACAGTGTGACTTCCGTGCTCAGTGTGCCGAGC 2083
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QY 2144 ATCAGACTTATGCAAACTCTACTGTATCGCAGAAAGATTGATTTCTTCTTCTTGT 2203
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QY 2204 CAAATAAAGTCAAAGATGGGACTCGCATGCTCGAGAGATAGCCGTAAATGTTGTATAGATG 2263
Db 2175 CCGCAAAAGTGAAGATGGAACCTCCCTGCTCCCAAAACAAAATGATGTTGTATGACG 2234
QY 2264 GGATATGTGAGAGATTGGATGTGACAAATGTCTTGGATCTGATGTCTGTTGAAGACGTCT 2323
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Db 2235 GGGTTGTGAACCTAGTGGGATGTGATCATGAACTAGGCTCTAAGACAGTTTCAGATGCTT 2294
QY 2324 GTGGGGTGTGTAACGGGAATTACTCAGCCCTGACAGATTACAGAGGGTCTCTACACCAAGC 2383
Db 2295 GTGGCGTTTGCAAGGTGATTAATTCAACTTGCAAGTTTATTAAGGCCCTGTACTCAACC 2354
QY 2384 ACCACACACCAACCAAGTATTAATCAGATGCTACCATTTCTTCTGAGCCCGGAGTATCC 2443
Db 2355 AGCATTAAGCAATGATTAATTAATCCGGTGTGATCATTTCCAGCTGGCGCCGAAACATCG 2414
QY 2444 GCATCTATGAATGAACGTCTTACTCTTACCTCTTACATTTCTGTGCGCAATGCCCCTCAGAAGT 2503
Db 2415 AAATCCAGAGCTGCAGGTTTCTCTCAGTTAACCCTGCAAGTTGAAAGCTCAAGTCAAAAGT 2474
QY 2504 ACTACCTGAATGGGCACCTGACCGGTGACCTGACCGCCCGGTACAAATTTTCGGGACCTA 2563
Db 2475 ATTAACCTACCGGGGCTGAGCATGCACTGCGCTGGGAGTTCCCTTCCGTGGACCA 2534
QY 2564 CTTTGCATACAGACGGTCTTATTAATGAGCCCGAGAACTTAATCGCTACTGACCAACCA 2623
Db 2535 CGTTTGAATACACGCGCTCTTCAACCGCCGGAACGTCTGTACCGCCAGGGCCACAA 2594
QY 2624 ACAGACACATGATTTGTGAGCTGTGTTTACAGGGAAGAACCCGGGTGTGCTGGGAAT 2683
Db 2595 ATGAGACGCTGTGCTTTGAATTTCTGATGCAAGGCAAAAATCCAGGATAGCTTGAAGT 2654
QY 2684 ACTCCATGCTCGCTTGGGGAACGAGAACCCCTGCCCA--GCCACGTACACTT 2740
Db 2655 ATGCACTTCCCAAGTCATGAATGGAACCTCACACGACCAAAAAGACCTGCTTATACC 2714
QY 2741 GGGCCATCGTGCCTCTGAGTGTCTCGTGTGCGAGGGGT 2784
Db 2715 GGAATATCGTCACTCAGAGTGTCTCCGTCTCTGTGTGAGGT 2758
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RESULT 14
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; Sequence 3, Application US/10354983
; Publication No. US20040044194A1
; GENERAL INFORMATION:
; APPLICANT: AGOSTINO, MICHAEL J.
; APPLICANT: CORCORAN, CHRISTOPHER
; TITLE OF INVENTION: AGGRECANASE MOLECULES
; FILE REFERENCE: 08702.0111-00000
; CURRENT APPLICATION NUMBER: US/10/354,983
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: 60/353,680
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3219
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-354-983-3
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Query Match 24.5%; Score 708; DB 18; length 3219;
Best local Similarity 64.9%; Pred. No. 3.8e-212;
Matches 1080; Conservative 0; Mismatches 580; Indels 4; Gaps 2;

QY 1124 AGACCTGTGTGTGTGTCGACAAAAGATGATGCAAAAACCATGGCCATGAAATATCACCA 1183
Db 945 AAACGTGTGTGTGTGAGCCTTAATCTTCTGGAACAAGAACCTGAGGATTAATGATCAA 1004
QY 1184 CCTACGTGCTCAGATATCTCAACATGTGTATCTGCTTTATTCAAAAGATGATGAGGGA 1243
Db 1005 CCATCATGCAACCAAGTCTCTGAATAGTTTTTG--TCAATGGCAGTCTGCCCTCATTTGAA 1063
QY 1244 AAGATGGGACTCGTATGACCAAGCCATCTTAAGTCTGCTGTGATATATGTTCTCTGA 1303
Db 1064 AGAATGGCAAGACATGATCATGCTTCTTAATAACAGAAATTTGATATTTGTTCTTGA 1123
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QY 1304 AGAATGAGCCCTGTGACACTTTGGGATTGCACCCATGAAGTGAATGTGTAAATATTC 1363
DB 1124 AGAATGAACCAATGTGACACTTAAGGGTTTGCCCCCATCAGTGAATGTGCTCTAAAGTACC 1183
QY 1364 GCAGCTGCACGATTAATGAAGATACAGGCTTTGGAGCTGGCCTTCAACCATGGCCATGAGT 1423
DB 1184 GAAAGTTGATCATCATGAGGACACAGGACTTGGCCTTGCTTCAACCATGCTCATGAGT 1243
QY 1424 CTGGACACAACCTTTGGCATGATTCATGATGAGAAGGAAACAATGTGTAAAAAGTCCGAGG 1483
DB 1244 CAGGGCAACAACCTTTGGTATGATTCACGACGGAGAAGGAAATCCCTGCAGAAAAGGCTGAAG 1303
QY 1484 GCAACATCATGTCCCTTACATTTGGCAGACGCAATGAGTCTTCTCTGTGCAACCTGCA 1543
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QY 1604 CAAGCCCTGTGAAGGAATACAGTATCTTGAGAAATTTGCCAGAGAATTAATATGATGCAA 1663
DB 1424 CCAAGCAAGCAGGACAGTATTAATATCCGGCAAACTACAGGACAGATTTATGATGCTG 1483
QY 1664 ACACACAGTGCAAGTGGCAGTTCGAGAGAAAGCCAAAGCTCTGATGCTGGACTTTAAAA 1723
DB 1484 ACACACAGTGTAAATGGCAATTTGGAGCAAAAGCCAAAGTTATGACGCTTGTGTTGTGA 1543
QY 1724 AGGACATCTGTAAAGCCCTGTGGTGGCCATCTGATTTGGAAGAAATGTGAGACTAAATTTA 1783
DB 1544 AGGATATTTGCAAAATCACTTTGGTGGCCACCGAGTAGGCCACAGGTGTGAAGCCAAATTTA 1603
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QY 1844 TGAATATATGTGATGAAGGCCCCCAAGCCCACTGAGGCTGAGTGTGCTGCTTCTT 1903
DB 1664 TAAAGTTTGGGAGCTCGGGCCCCGGCCCAATCCAAGGAGTGTGCTGCTGCTGCAAGT 1723
QY 1904 GGTCCCCATGCTCCAGACCTGCGAGGGGAGTATCTCATAGAGTGCCTCTGCACCA 1963
DB 1724 GGTCAGAATGTTCGCCGACATGTGTGAGAGTCAAGTTCAGAGAGACACTGCAATA 1783
QY 1964 ACCCCAAAGCCATCGCATGAGGAGAAAGTTCTGTGAGGGCTCCACTGCACTTGAAGCTCT 2023
DB 1784 ACCCCAAAGCCTCAGTATGTGTGACATATTTCTGTCCAGTTTCAAGCTTATTAACAGCTGT 1843
QY 2024 GCAACAGTCAGAAATGTCCCGGGGACAGTGTGACTTCCGTGCTGCTCAGTGTGCCGAGC 2083
DB 1844 GCAATATTAACCTTTCGATGAATAATAGCTTGGATTTTCGGGCCCAACAGAGTGCAGAAAT 1903
QY 2084 ACAACAGCAGACGATTCAGAGGGGCGGACATCAAGTGAAGCCTTACACTCAAGTAGAAG 2143
DB 1904 ATAAACAGCAAACTTTCCGTGGATGTTCTTACCAAGTGAACCTATACAAGAGTGAAG 1963
QY 2144 ATCAGGACTTATGCAAACTCTACTGTATCGAGAAGATTGATTTCTTCTTTCTTTGT 2203
DB 1964 AGGAAGATCATGCAAACTGTACTGCAAGGCTGAAGAACTTGAATTTTGTGCAATGT 2023
QY 2204 CAAATAAAGTCAAAAGATGGGACTCCATGCTCGGAGAGTAGCCGTAATGTTGTATAGATG 2263
DB 2024 CCGGCAAAAGTGAAGATGGAATCCCTGCTCCCAAAACAGAAATGATGTTGTATGACG 2083
QY 2264 GGATATGTGAGAGATGTGATGTGACAATGTCTTGTGATGATGCTGTGGAAGAGCTCT 2323
DB 2084 GGGTTTGTGAATAAGTGGATGTGATCATGAATAAGCTTAAGCAGATTCAAGATGCTT 2143
QY 2324 GTGGGCTGTGAACGGGAATTAATCAGCCTGCACGATTCACAGGGGTCTCTACACCAAGC 2383
DB 2144 GTGGCTTTGCAAAAGGTGATTAATTCACCTTGCAAGTTTATTAAGGCCCTGTACTCAACC 2203
QY 2384 ACCACCAACCAACAGTATTAATCATATGTGTACCATTTCTTCTGAGCCCGGAGTATCC 2443

DB 2204 AGCATTAAGCAATGATATATATATCCGGTGTGTCATATTCAGCTGGCGCCCGAAGCATCG 2263
QY 2444 GCATCTATGAATGAACGCTCTCTACCTCTCTACATTTCTGTGGCAGATGCCCTCAGAAAGT 2503
DB 2264 AAATCCAGAGCTGCAGGTTTCTCTCCAGTTAACCTCGCAGTTCCGAAGCCTCAGTCAAAAGT 2323
QY 2504 ACTACCTGAATGGGCACTGGACCGGTGACTGGCCCGCCGGTACAAATTTTCGGGCACTA 2563
DB 2324 ATTACCTTCAACCGGGGCTGGAGCATCGACTGGCCTGGGAGTTCCCTTCGCTGGGACCA 2383
QY 2564 CTTTGCATAACAGACGGTCTTATATGAGCCCGAGAACTTAATGCTTACTGGAACCA 2623
DB 2384 CGTTGAAATACCAAGCGCTCTTTCACACCGCCCGGAAACGTCTGTACGCGCCAGGGCCCA 2443
QY 2624 ACAGACACTGATTTGTGAGCTGCTGTTTCAAGGAAAGAACCCGGGTGTGCTGGGAAT 2683
DB 2444 ATGAGACGCTGTCTTTGAAATTTCTGATGCAGGCAAAATCCAGGGATAGCTTGGAAAT 2503
QY 2684 ACTCCATGCTCGCTTGGGGACCGAGAACAGCCCGCTGCCCA--GCCCACTACACTT 2740
DB 2504 ATGACCTTCCCAAGGTCAATGAATGAACTCCACAGCCACAAAGAACCTGCTTATACCT 2563
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RESULT 15
US-10-354-983-1
; Sequence 1, Application US/10354983
; Publication No. US20040044194A1
; GENERAL INFORMATION:
; APPLICANT: AGOSTINO, MICHAEL J.
; APPLICANT: CORCORAN, CHRISTOPHER
; TITLE OF INVENTION: AGGREGANASE MOLECULES
; FILE REFERENCE: 08702.0111-00000
; CURRENT APPLICATION NUMBER: US/10/354, 983
; PRIOR FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: 60/353, 680
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3663
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-354-983-1

Query Match 24.5%; Score 708; DB 18; Length 3663;
Best Local Similarity 64.9%; Pred. No. 4.1e-212;
Matches 1080; Conservative 0; Mismatches 580; Indels 4; Gaps 2;
QY 1124 AGACCTTGGTGGTGTGACAAAAGATGATGCAAAACCATGGCCATGAAAAATATCACCA 1183
DB 1014 AAACGTGGTGTGTGAGCCTTAATTCCTCTGGAACAGAACTGAGAGTTATTGATCAA 1073
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DB 1074 CCATCATGCAACCACTCTCGAATAGTTTGTG-TCATGCGAGTGTGCCCTCATTTGAA 1132
QY 1244 AAGATGGGACTGTCATGACCAACGCCATCTTACTGACTGTCTGATATATGTTCCCTGA 1303
DB 1133 AGAATGGCAAGAGACATGATCATGCTTACTTAACAGGATTTGATTAATTTGTTCTTGA 1192
QY 1304 AGAATGAGCCCTGTGACACTTTGGGATTTGCAACCAATAAGTGAATGTAGTAAATATC 1363
DB 1193 AGAATGAACCATGTGACACTTAAGGTTTGGCCCCCATCAAGTGAATGTCTTAAGTACC 1252
QY 1364 GCAGCTGCACGATTAATGAAGATACAGGTCTTGAAGCTGGCCTTACCATGCCCCATGAGT 1423
DB 1253 GAAAGTTTACATCATGAGGACACAGGAACTTGGCCTTGCCTTACCATGCTCATGAGT 1312

QY	1424	CTGGACACAACTTTGGCATGATTCATGATGGAGAGGGAA	CACTGTGTAAAAAGTCCGAGG	1483				
Db	1313	CAGGGCACAACTTTGGTATGATTCACGACGGAGAGGGAA	TCCCTGCAGAAAGGCTGAAG	1372				
QY	1484	GCAACATCATGTCCCTACATTGGCAGAGCGCAATGGAG	TCCTCTCTGCTCACCCCTGCA	1543				
Db	1373	GCAATATCATGTCTCCACACTGACCCGGAAACA	TGAGTGTCTTTCATGTCTTCTTGCA	1432				
QY	1544	GCCGCCAGTATCTACACAAATTTCTAAGCACCCGCT	CAAGCTATCTGCCTTGCTGATCAGC	1603				
Db	1433	GCCGCCAGTATCTCAAGAAATTCCTCAGCACACCT	CAGCGGGGTGTCTAGTGGATGAGC	1492				
QY	1604	CAAAGCCTGTGAAGGAATACAAAGTATCCTGAGAA	ATTGGCCAGAGAAATTATATGATGCAA	1663				
Db	1493	CCAAGCAAGCAGAGCAGTATAAATATCCGGACAA	CTACCAGGACAGATTTATGATGCTG	1552				
QY	1664	ACACACAGTGCAAAGTGGCAGTTCCGAGAGAGAA	AGCCAAAGCTCTGCATGCTGCACTTTAAAA	1723				
Db	1553	ACACACAGTGTAAATGGCAATTTGGAGCAAAAG	CCAAAGTTATGCAAGCCTTGTGTTTGTGA	1612				
QY	1724	AGGACATCTGTAAAGCCCTGTGTGTCATCGTAT	TGGAAAGCAATGTGAGACTAAATTTTA	1783				
Db	1613	AGGATATTTGCAAAATCACTTTGTGTCACCCGAG	TAGGCCACAGGTGTGAGACCAAGTTTA	1672				
QY	1784	TGCCAGCAGCAGAAAGGCACAAATTTGTGGGCA	TGACATGTGTGTCGGGGAGGACAGTGTG	1843				
Db	1673	TGCCCGCAGCAGAAAGGACCCGTTTGTGCTTG	AGTATGTGTGTGCGCAAGGCCAGTGGC	1732				
QY	1844	TGAATATATGTGTGATGAAAGGCCCCAAAGCC	CAACCCATGCGCCACTGCTGCTCTTCTT	1903				
Db	1733	TAAAGTTTGGGAGAGCTCGGGCCCCCGGCCA	TCCAGTGTGTGCTGCTGCTGCTGCTG	1792				
QY	1904	GGTCCCCATGCTCCAGGACCTGCGGAGGGGGAG	TATCTCATAGGAGTGCCTCTGCACCA	1963				
Db	1793	GGTCAGAAATGTTCCCGGACATGTGTGTGAGAG	GTCAAGTTCACAGAGAGACACTGCATA	1852				
QY	1964	ACCCCAAGCCATCGCATGAGAGGGAAGTTCT	GTGAGGGCTCCA	CTGCAC	CTGAAAGCTCT	2023		
Db	1853	ACCCCAAGCCTCAGTATGTGTGTCATATTC	GTGCCAGGTTCT	AGCCGTA	TTTATCAGCTGT	1912		
QY	2024	GCAACAGTCAGAAATGTCCCGGGACAGTGTGA	CTTCCGCTGCTC	CAGTGTG	CCGAGC	2083		
Db	1913	GCAATATTAACCTTGCAATGAAATAAGCTTGA	TTTCCGGGCCA	CAGTGTG	CAGAA	1972		
QY	2084	ACAAACAGCAGACGATTCAGAGGGCGGCAC	TACAAAGTGAAGC	CTTAC	CTCACTCA	AGTAGAAG	2143	
Db	1973	ATAACAGCAAACTTTCCGTGATGGTTCT	ACAGTGAAC	CCCTA	TACAAAA	AGTGAAG	2032	
QY	2144	ATCAGGACTTATGCAAACTCTACTGTATCGCA	GAAGATTGA	TTTCTTCTT	CTTCTT	CTTGT	2203	
Db	2033	AGGAAAGATCGATGCAAACTGTACTGCAAGG	CTGAGAACTTGA	ATTTTTTTT	TTTGCAATGT	2092		
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Db	2153	GGGTTTGTGAAGTATGTGGAGTGTGATCAT	GAACTAGGCT	CTAAAGCAG	TTTCA	GATGCTT	2212	
QY	2324	GTGGGGTGTGTACCGGGAATTA	CTCAGCC	TGCAAGATTCA	CAGGGGTCT	CTACACCAAGC	2383	
Db	2213	GTGGCGTTTGCAAAGGTGATTAATCA	CTTGCAAGTTT	TATAAAGCC	CTGTAC	CTCAACC	2272	
QY	2384	ACCACCAACCAACCAAGTATTA	TCACATGTGTCA	CCATTCCTT	CTGAGCCCGGAG	TATCC	2443	
Db	2273	AGCATTAAGCAAAATGAATATTA	TATCCGGTGTCA	TCAATTCAG	GTGGCGCCGGAAG	CATCG	2332	
QY	2444	GCAATCTATGAATGAACGTC	CTCTACCTC	CTACATTTCT	GTGTGGCAATG	CCCTCAGAAAGT	2503	
Db	2333	AAATTCAGAGAGCTGCAAGTTTCT	CTCCAGTTAC	CTGCAAGTT	CGAAAGCCTCAGT	CAAAAGT	2392	
QY	2504	ACTA	CTGAAATGGGCACTG	GACGCTG	AGCTG	CGCCCGCGGTACA	AAATTTTCCGGGCACTA	2563

Db	2393	ATTACCTCACCGGGGGCTGGAGCATCGACTGGCTGGGAGTTCCTCGCTGGAGCA	2452
QY	2564	CTTTCGACTACAGACGTCCTATATGAGCCGAGAACTTAATCGCTACTGACCAACA	2623
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QY	2624	ACGAGACACTGATTTGTGAGCTGCTGTTTCAGGGAAGAACCCGGGTGTTCCTGGAA	2683
Db	2513	ATGAGACCGTGGTCTTTGAAATTTCTGATGCAAGCAAAATCCAGGATAGCTTGAAGT	2572
QY	2684	ACTCCATGCTTCGCTTGGGACCGAGAGCAAGCCCCCTGCCA--GCCCACTACACTT	2740
Db	2573	ATGCACTTCCCAAGGTCATGAAATGGAACTCCACCAAGCCACAAAAAGACCTGCCTATACCT	2632
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 9, 2005, 02:13:13 ; Search time 492 Seconds
(without alignments)
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Gapop 10_0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1874.6	64.8	3675	3	US-09-930-872-3	Sequence 3, Appli
2	1874.6	64.8	3675	4	US-10-217-774-3	Sequence 3, Appli
3	1874.6	64.8	4042	3	US-09-930-872-5	Sequence 5, Appli
4	1874.6	64.8	4042	4	US-10-217-774-5	Sequence 5, Appli
5	663	22.9	1476	3	US-09-930-872-1	Sequence 1, Appli
6	663	22.9	1476	4	US-10-217-774-1	Sequence 1, Appli
7	227	7.8	2274	4	US-09-963-791-23	Sequence 23, Appli
8	227	7.8	2274	4	US-09-963-791-1	Sequence 1, Appli
9	209.6	7.2	3571	4	US-09-799-451-411	Sequence 411, App
10	206.4	7.1	3377	4	US-09-981-953A-3	Sequence 3, Appli
11	204.6	7.1	5357	3	US-09-392-184-5	Sequence 5, Appli
12	201.6	7.0	3766	4	US-09-981-953A-1	Sequence 1, Appli
13	182.6	6.3	3218	3	US-09-369-364A-6	Sequence 6, Appli
14	176.8	5.0	3885	3	US-09-369-364A-16	Sequence 16, Appli
15	144	4.2	2848	3	US-09-369-364A-4	Sequence 4, Appli
16	123	4.2	3160	4	US-09-963-791-25	Sequence 25, Appli
17	118.4	4.1	2450	3	US-09-963-791-2	Sequence 2, Appli
18	118.4	4.1	6692	3	US-09-491-522-1	Sequence 1, Appli
19	118	4.1	1317	4	US-09-963-791-21	Sequence 21, Appli
20	118	4.1	1770	4	US-09-963-791-11	Sequence 11, Appli
21	116.8	4.0	3636	4	US-09-949-016-5530	Sequence 5530, Ap
22	114.2	3.9	2450	3	US-09-491-522-9	Sequence 9, Appli
23	114.2	3.9	4580	3	US-09-491-522-8	Sequence 8, Appli
24	113.6	3.9	5804	3	US-09-369-364A-12	Sequence 12, Appli
25	110	3.8	2853	4	US-10-009-332-2	Sequence 2, Appli
26	102.6	3.5	1071	4	US-09-963-791-19	Sequence 19, Appli
27	102.6	3.5	1524	4	US-09-963-791-9	Sequence 9, Appli

28	102.4	3.5	3002	3	US-09-369-364A-1	Sequence 1, Appli
29	101.2	3.5	2184	4	US-09-445-023A-13	Sequence 13, Appli
30	97.2	3.4	3706	3	US-09-484-970B-58	Sequence 58, Appli
31	97.2	3.4	4676	3	US-09-130-491-1	Sequence 1, Appli
32	97.2	3.4	4858	3	US-09-392-184-1	Sequence 1, Appli
33	95.6	3.3	3889	4	US-09-568-559-1	Sequence 2, Appli
34	94	3.2	2184	4	US-09-445-023A-2	Sequence 15, Appli
35	91.6	3.2	954	4	US-09-963-791-15	Sequence 5, Appli
36	91.6	3.2	1407	4	US-09-963-791-5	Sequence 14, Appli
37	85.4	2.9	6659	4	US-09-321-987B-1	Sequence 8, Appli
38	85.2	2.9	2625	3	US-09-369-364A-14	Sequence 14, Appli
39	85.2	2.9	3638	3	US-09-122-126B-14	Sequence 14, Appli
40	83.6	2.9	3250	3	US-09-634-286A-14	Sequence 14, Appli
41	83.6	2.9	3250	4	US-10-247-685-14	Sequence 14, Appli
42	83.6	2.9	3250	4	US-10-247-685-14	Sequence 16352, A
43	80.4	2.8	601	4	US-09-949-016-164396	Sequence 16352, A
44	80.4	2.8	56147	4	US-09-949-016-16352	Sequence 16600, A
45	80.4	2.8	298336	4	US-09-949-016-16600	

ALIGNMENTS

RESULT 1									
US-09-930-872-3									
; Sequence 3, Application US/09930872									
; Patent No. 6448388									
; GENERAL INFORMATION:									
; APPLICANT: Friddle, Carl Johan									
; APPLICANT: Hilbun, Erin									
; TITLE OF INVENTION: No. 6448388e1 Human Proteases and Polynucleotides Encoding the San									
; FILE REFERENCE: LEX-0219-USA									
; CURRENT APPLICATION NUMBER: US/09/930,872									
; CURRENT FILING DATE: 2001-08-14									
; PRIOR APPLICATION NUMBER: US 60/225,852									
; PRIOR FILING DATE: 2000-08-16									
; NUMBER OF SEQ ID NOS: 5									
; SOFTWARE: FastSeq for Windows Version 4.0									
; SEQ ID NO 3									
; LENGTH: 3675									
; TYPE: DNA									
; ORGANISM: homo sapiens									
US-09-930-872-3									
Query Match 64.8%; Score 1874.6; DB 3; Length 3675;									
Best Local Similarity 84.4%; Pred. No. 0;									
Matches 2287; Conservative 0; Mismatches 179; Indels 245; Gaps 6;									
QY	202	GCAGGACCTGGCTGCGCCATGGAGACCCGCGGCGAGCGCGCTGGGAGCCCGACGCTCC	261						
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QY	262	GCGTCTCTCTCCACCGCGGAGCGCGCGCTGGATGGAAGGGCGGACATGATGAA	321						
DB	129	GCGTCTCTCTCCACCGCGGAGCGCGCGCTGGATGGAAGGGCGGACATGATGAA	175						
QY	322	GCTGAAACCATCTGTTCTCAGCAACTAACAGGAACAAACCAACTGATGTT	381						
DB	176	-----AAATGACCTGGTCTCTGCTACGAGGTGACCAAGGGCGATTAAGTCTC	175						
QY	382	CTCACTCAATATGACCTGCTCTGCTACGAGGTGACCAAGGGCGATTAAGTCTC	441						
DB	176	-----AAATGACCTGGTCTCTGCTACGAGGTGACCAAGGGCGATTAAGTCTC	228						
QY	442	CATGAATCATGACCATCAGCGCGGAGAGAGCAGTGGCGGTGCCAGGTGAGTCT	501						
DB	229	CATGAATCATGACCATCAGCGCGGAGAGAGCAGTGGCGGTGCCAGGTGAGTCT	288						
QY	502	CTTACCTTCGCTGAAAGGCCCGAGGACGACTTCCACATGATCTGAGGACTCCAGC	561						
DB	289	CTTACCTTCGCTGAAAGGCCCGAGGACGACTTCCACATGATCTGAGGACTCCAGC	348						
QY	562	AGCCTAGTGGCTCTGCTTATTTGTGACAGCTTGGAAAGACAGGACCTAAGTCTGTG	621						

Db 349 AGCCTAGTGCTCCTGGCTTTATTTGTCAGACGTTGGGAAAGACAGGCACCTAAGTCTGTG 408
QY 622 CAGACTTTACCGCAGAGGACTTCTGTTTCTATCAAGGCTCTTGGCATCACAGAAAC 681
Db 409 CAGACTTTACCGCAGAGGACTTCTGTTTCTATCAAGGCTCTTGGCATCACAGAAAC 468
QY 682 TCGCCATCGCATGAGGAGGAACTTCTGTGAGGCTCCACTCGCACTCTGAAGCTTGCAAC 741
Db 469 TCTCTCA-----GTGGCCCTTCAACCTGCCAAGGCTTGTCA 504
QY 742 ACTCAGAAATGTCCCCGGGACAGGTGTGACTTCCGTGCTGCTCAAGTGTGCCGACACAAC 801
Db 505 GGCATGATACGAACAGAAAGGCGATTACTTCTTAAGGCCACTTCTTCAACACTCTCA 564
QY 802 AGCAGACGATTTCAGAGGGCGGCACTACAAGTGG--AAGCCTTACACTCAAGTAGAAGCCG 859
Db 565 TGGAAACTCGGCGAGAGCTGCCCAAGGCAAGCTCGCCATCCCAAGTACTGTACAGAGATCC 624
QY 860 ACTTATGCAAACTCTACTGTATCGCAGAAAGGATTGATTCTTCTTTCTTTGTCAATA 919
Db 625 ACAGAGCCCCCATGCTCCTGGGGCAGTGAGGTCTGTGACCTC-----AAGG 672
QY 920 AAGTCAAAAGATGGGACTCCATGCTCGGAGGATAGCCGTAATGTTTGTATAGATGGGATAT 979
Db 673 ACATGGGAGCTGGCACATCAACCCCTGCACAGACGCAACCTTGCCCTGGGACTGCCACAA 732
QY 980 GTGAGCTCAGTGTGTGTGTCCACACTGTGC-GCACAATGCCCCAGCCTCCCAAGAAAGCCTC 1038
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QY 1039 TTTCATCTTGGCAGATGAGTATAGTCTTGTCTTAACGGCATTAAGCGCTCTCTTGTAGGTCC 1098
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QY 1099 CATAGAAATGAAGAAGTGAACGTGAGAGACCTTGGTGTGTGTCGACAAAGATGATGCAA 1158
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QY 1159 AACCATGGCCATGAAAATATCAACCTACGTCCTCACGATCTCAACATGGTATCTGCT 1218
Db 913 AACCATGGCCATGAAAATATCAACCTACGTCCTCACGATCTCAACATGGTATCTGCT 972
QY 1219 TTATTCAAGA----- 1229
Db 973 TTATTCAAGAATGGAACAATAGAGAAACATCAACATTGCAATTGTAGTCTGATTCTT 1032
QY 1230 ----- 1229
Db 1033 CTAGAAGATGAACAGCCAGACTGTGATAGTCAACCAACGACACCACTTAAAGTAGC 1092
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Db 1093 TTCTGCCAGTGGCAGTCTGGAATTGATGGGGAAGAATGGGACTCGTCATGACCAAGCCCATC 1152
QY 1273 TTACTGACTGGTCTGGATATATGTTCTCTGGAAGAATGAGCCCTGTGACACTTTTGGGATTT 1332
Db 1153 TTACTGACTGGTCTGGATATATGTTCTCTGGAAGAATGAGCCCTGTGACACTTTTGGGATTT 1212
QY 1333 GCAACCATTAAGTGAATGTGTAGTAATAATGCGAGCTGCAGCATTAATGAAGATACAGGT 1392
Db 1213 GCAACCATTAAGTGAATGTGTAGTAATAATGCGAGCTGCAGCATTAATGAAGATACAGGT 1272
QY 1393 CTGAGACTGGCCTTACCAATTGCCATGAGTCTGGAACAACCTTGGCATGATTCATGAT 1452
Db 1273 CTGAGACTGGCCTTACCAATTGCCATGAGTCTGGAACAACCTTGGCATGATTCATGAT 1332
QY 1453 GGAGAAAGGGAACATGTGTAAAAAGTCCGAGGGCAACATCATGTCCCTACATTTGGCAGGA 1512
Db 1333 GGAGAAAGGGAACATGTGTAAAAAGTCCGAGGGCAACATCATGTCCCTACATTTGGCAGGA 1392
QY 1513 CGCAATGAGTCTTCTCTGCTGTCACCTGCGAGCCGCGCATATCTACACAAATTCTAAGC 1572
^

Db 1393 CGCAATGAGTCTTCTCTGCTGTCACCCCTGCAGCCGCGCATATCTACACAAATTCTAAGC 1452
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Db 1453 ACCGCTCAAGCTATCTGCTCTGCTGATCAGCCAAAGCCTGTGAAGAAATCAAGTATCCT 1512
QY 1633 GAGAAATTGCCAGAGAAATTATATGATGCAAAACACAGTGCAGAGTGGCAGTTCGAGAG 1692
Db 1513 GAGAAATTGCCAGAGAAATTATATGATGCAAAACACAGTGCAGAGTGGCAGTTCGAGAG 1572
QY 1693 AAAGCCAAGCTCTGCATGCTGACTTTAAAAAGACATCTGTAAAGCCCTGTGTGCCAT 1752
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QY 1753 CGTATTGGAAGGAATGTGAGACTAAATTATGCCAGACAGAAAGGCACAATTGTGGG 1812
Db 1633 CGTATTGGAAGGAATGTGAGACTAAATTATGCCAGACAGAAAGGCACAATTGTGGG 1692
QY 1813 CATGACATGTGTGCGGGGAGGACAGTGTGTAATAATGTGTATGAAGCCCCCAAGCCC 1872
Db 1693 CATGACATGTGTGCGGGGAGGACAGTGTGTAATAATGTGTATGAAGCCCCCAAGCCC 1752
QY 1873 ACCCATGGCCACTGTCGGAAGTGTCTTCTTGTGTCGCCATGCTCCAAGACCTGCGAGGG 1932
Db 1753 ACCCATGGCCACTGTCGGAAGTGTCTTCTTGTGTCGCCATGCTCCAAGACCTGCGAGGG 1812
QY 1933 GGAGTATCTCATAGAGTGTGCTCTGCAACCAACCCCAAGCCATCGCATGGAAGGAAGTTC 1992
Db 1813 GGAGTATCTCATAGAGTGTGCTCTGCAACCAACCCCAAGCCATCGCATGGAAGGAAGTTC 1872
QY 1993 TGTAGGGCTCCACTCGCACTCTGAAGCTCTGCAACAGTCAAGAAATGTCCCCGGGACAGT 2052
Db 1873 TGTAGGGCTCCACTCGCACTCTGAAGCTCTGCAACAGTCAAGAAATGTCCCCGGGACAGT 1932
QY 2053 GTTGACTTCCGTGCTGCTCAGTGTGCGGAGCACAAAGCAGATTCAGAGGGCGGAC 2112
Db 1933 GTTGACTTCCGTGCTGCTCAGTGTGCGGAGCACAAAGCAGATTCAGAGGGCGGAC 1992
QY 2113 TACAAGTGAAGCCTTACACTCAAGTGAAGATCAGGACTTATGCAAACTCTACTGTATC 2172
Db 1993 TACAAGTGAAGCCTTACACTCAAGTGAAGATCAGGACTTATGCAAACTCTACTGTATC 2052
QY 2173 GCAGAGGATTTGATTTCTTCTTTCTTGTCAAAATAAAGTCAAAAGTGGGACTCCATGC 2232
Db 2053 GCAGAGGATTTGATTTCTTCTTTCTTGTCAAAATAAAGTCAAAAGTGGGACTCCATGC 2112
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Db 2173 GTCCTTGGATCTGATGCTGTGTAAGACGTCTGTGGGTGTGTAAACGGGAATACTCAGCC 2232
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Db 2293 GTCAACATTCTTCTGGAAGCCCGGAGTATCCGCATCTATGAAATGAACGTCTTACCTCC 2352
QY 2473 TACATTTCTGTGCGCAATGCCCTCAGAAAGTACTACCTGAATGGGCACTGGAACGCTGAC 2532
Db 2353 TACATTTCTGTGCGCAATGCCCTCAGAAAGTACTACCTGAATGGGCACTGGAACGCTGAC 2412
QY 2533 TGGCCCGCCGGTACAAATTTTGGGCACTACTTTCGACTACAGACGCTCTATATGAG 2592
Db 2413 TGGCCCGCCGGTACAAATTTTGGGCACTACTTTCGACTACAGACGCTCTATATGAG 2472
QY 2593 CCGGAGAACTTAATCGCTACTGACCAACCAACGAGACACTGATTGTGAGAGCTGCTGTTT 2652
Db 2473 CCGGAGAACTTAATCGCTACTGACCAACCAACGAGACACTGATTGTGAGAGCTGCTGTTT 2532

QY	2653	CAGGGAAAGAACCCGGG	GTGGCTGGGAAT	CTCCATGCTCGCTTGGGGA	CCGAGAA	2712
Db	2533	CAGGGAAGAACCCGGG <td>TGTGCTGGAA</td> <td>TACTCATGCTTCGCTTGGGGA <td>CCGAGAA <td>2592</td> </td></td>	TGTGCTGGAA	TACTCATGCTTCGCTTGGGGA <td>CCGAGAA <td>2592</td> </td>	CCGAGAA <td>2592</td>	2592
QY	2713	CAGCCCCCTGCCCAGCC	AGCTACCTTGGGCCAT	CGTGTGCTCTGAGTGTCCGTCC		2772
Db	2593	CAGCCCCCTGCCCAGCC	AGCTACCTTGGGCCAT	CGTGTGCTCTGAGTGTCCGTCC		2652
QY	2773	TGCGGAGGGG				
Db	2653	TGCGGAGGGG				

RESULT 2
US-10-217-774-3
; Sequence 3, Application US/10217774

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; GENERAL INFORMATION:
; APPLICANT: Fridde, Carl Johan
; APPLICANT: Hilbun, Erin
; TITLE OF INVENTION: No. 6734007e1 Human Proteases and Polynucleotides Encoding the
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0219-USA
; CURRENT APPLICATION NUMBER: US/10/217,774
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US/09/930,872
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,852
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3675
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-217-774-3

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Query Match	64.8%;	Score 1874.6;	DB 4;	Length 3675;
Best Local Similarity	84.4%;	Pred. No. 0;		
Matches 2287; Conservative	0;	Mismatches 179;	Indels 245;	Gaps 6;

[illegible]

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QY	742	AGTCAGAAATGTCCTCCGGACAGTGTGACTTCCGTGCTGCTCAGTGTGCCGACACAAC	801
Db	505	GGCATGATACGAACAGAAAGGACAGATTACTTCTTAAGGCCACTTCTTCACACCTCTCA	564
QY	802	AGCAGACGATTTCAGAGGGCGGCACTACAAGTGG--AAGCCTTACACTCAAGTAGAAGCCG	859
Db	565	TGGAAACTCGGCAGAGCTGCCCAAGGCAGCTCGCCATCCCAAGTACTGTACAGAAGATCC	624
QY	860	ACTTATGCAAACTCTACTGTATCGCAGAAGGATTGATTTCTTTCTTTGTCAATA	919
Db	625	ACAGAGCCCCATGCTCTCTGGGGCCAGTAGGGTCTGTGACCTC-----AAGG	672
QY	920	AAGTCMAAGATGGGACTCCATGCTCGAGGATAGCCGTAATGTTGTATAGTGGGATAT	979
Db	673	ACATGGAGCTGGCACAATCAACCCCTGCACAGCAGCAACCTTCGCCCTGGGACTGCCACAA	732
QY	980	GTGAGCTCAGTGTGTGTCCACATCTGC-GCACAATGCCCGCCAGCTCCCAAGGAAGACCTC	1038
Db	733	AAGCAGCATTTCTGTGGAAGACGCAAGAAATACATGCCCCAGCCTCCCAAGGAAGACCTC	792
QY	1039	TTTCATCTTGGCAGATGAGTATAGTCTTGTCTTACGGCATAAAGCGCTCTCTTCGAGGTCC	1098
Db	793	TTTCATCTTGGCAGATGAGTATAGTCTTGTCTTACGGCATAAAGCGCTCTCTTCGAGGTCC	852
QY	1099	CATAGAAATGAAGAAGCTGAACGTGGAGACCTTGTGTGTGTGACAAAAGATGATGCAA	1158
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QY	1159	AACCATGGCCATGAAAATATACCAACCTAGCTGCTCACGATCTCAACATGSTATCTGCT	1218
Db	913	AACCATGGCCATGAAAATATACCAACCTAGCTGCTCACGATCTCAACATGSTATCTGCT	972
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Db	973	TTATTCAAGATGGAACAATAGAGGAACAATCAATTGCAATTGTAGTCTGATTCTT	1032
QY	1230	-----	1229
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QY	1230	-----TGAATTGATGGGGAAGAATGGGACTCGTCATGACACGCCATC	1272
Db	1093	TTCTGCCAGTGGCAGTCTGGAATTGATGGGGAAGAATGGGACTCGTCATGACACGCCATC	1152
QY	1273	TTACTGACTGGTCTGATATATATGTTCTCGAAGAATGAGCCCTGTGACACTTTGGGATTT	1332
Db	1153	TTACTGACTGGTCTGATATATATGTTCTCGAAGAATGAGCCCTGTGACACTTTGGGATTT	1212
QY	1333	GCACCCATAGTGAATGTGTAAATATCGCAGCTGCAAGATTAAATGAATACAGGT	1392
Db	1213	GCACCCATAGTGAATGTGTAAATATCGCAGCTGCAAGATTAAATGAATACAGGT	1272
QY	1393	CTTGAAGTGGCTTCAACCATGGCCATGAGTCTGGAACAACCTTTGGCATGATTCATGAT	1452
Db	1273	CTTGAAGTGGCTTCAACCATGGCCATGAGTCTGGAACAACCTTTGGCATGATTCATGAT	1332
QY	1453	GGAGAAGGGAACATGTGTAAAGTCCGAGGGCAACATGATGTCCTTACATTGGCAGGA	1512
Db	1333	GGAGAAGGGAACATGTGTAAAGTCCGAGGGCAACATGATGTCCTTACATTGGCAGGA	1392
QY	1513	CGCAATGAGTCTTCTCCTGGTCAACCTGAGCCGCAAGTATCTACACAAATTTCTAAGC	1572
Db	1393	CGCAATGAGTCTTCTCCTGGTCAACCTGAGCCGCAAGTATCTACACAAATTTCTAAGC	1452
QY	1573	ACCGCTCAAGCTATCTGCTTGTGATCAGCCAAAGCCTGTGAAGGAATCAAGTATCCT	1632
Db	1453	ACCGCTCAAGCTATCTGCTTGTGATCAGCCAAAGCCTGTGAAGGAATCAAGTATCCT	1512

QY		920	AAGTCMAAAGATGGGACTCCCATGCCTCGAGAGATAGCCCCTAAATGTTTGTATAGATGGGATAT	979
Db		673	ACATGGGAGCTGGCACATCAACCCCTGCACACGACGACCCTTCCGCTGGGACTGCCACAA	732
QY		980	GTGAGCTCAGTGTGTGTGTCCACATCTGC - GCACATGCCCCAGCCTCCCAAGGAAGACCTC	1038
Db		733	AAGCAGCATTTCTGTGGAAGA GCGAAGAAATA CATGCCCCAGCCTCCCAAGGAAGACCTC	792
QY		1039	TTTCATCTTGCCAGATGAGTATTAAGTCTTGCTTAA CGGCATTAAGCGCTCTCTTCTGAGGTCC	1098
Db		793	TTTCATCTTGCCAGATGAGTATTAAGTCTTGCTTAA CGGCATTAAGCGCTCTCTTCTGAGGTCC	852
QY		1099	CATAGAAATGAAGA ACTGAA C GTGAGACCTTG TGTGTGTGCA CA AAA AGATGATGCAA	1158
Db		853	CATAGAAATGAAGA ACTGAA C GTGAGACCTTG TGTGTGTGCA CA AAA AGATGATGCAA	912
QY		1159	AAACCATGGCCATGAAAAATATCA CCACCTAGCTGCTCA CGA TACTCA ACATGGTATCTGCT	1218
Db		913	AAACCATGGCCATGAAAAATATCA CCACCTAGCTGCTCA CGA TACTCA ACATGGTATCTGCT	972
QY		1219	TTATTCAAGA -----	1229
Db		973	TTATTCAAGAATGGAACAATAAGAGAAAACATCAACATTGCAATTGTAGTCTGATTCTT	1032
QY		1230	-----	1229
Db		1033	CTAGAAGATGAACAGCCAGGACTGTGATTAAGTCACCA CGCAGACCA CACTTAAGTAGC	1092
QY		1230	-----TG AATTGATGGGGA AAGATGGGACTCGTCATGACAGCCCATC	1272
Db		1093	TTCTGCCAGTGGCAGTCTGGA TTGATGGGAAAAGATGGGACTCGTCATGACAGCCCATC	1152
QY		1273	TTACTGACTGGTCTGATATATATGTTCTCGA AAGATGAGCCCTGTGACACTTTGGGATTT	1332
Db		1153	TTACTGACTGGTCTGATATATATGTTCTCGA AAGATGAGCCCTGTGACACTTTGGGATTT	1212
QY		1333	GCACCCATAGTGAATGTGTAGTAATAATCGCAGCTGCA CGATTAA TGAAATACAGGT	1392
Db		1213	GCACCCATAGTGAATGTGTAGTAATAATCGCAGCTGCA CGATTAA TGAAATACAGGT	1272
QY		1393	CTTGACTGGCCTTCA CCA FTGCCATGAGTCTGGA CACA ACTTTGGCATGATTCATGAT	1452
Db		1273	CTTGACTGGCCTTCA CCA FTGCCATGAGTCTGGA CACA ACTTTGGCATGATTCATGAT	1332
QY		1453	GGAGAA GGGAACATGTGTAAAAAGTCCGAGGGCAACATCATGTCCCTACATTGGCAGGA	1512
Db		1333	GGAGAA GGGAACATGTGTAAAAAGTCCGAGGGCAACATCATGTCCCTACATTGGCAGGA	1392
QY		1513	CGCAATGAGACTTCTCTCCTGGTCA C C CTGAGCCG C CAGTATCTACACA AATTTCTAAGC	1572
Db		1393	CGCAATGAGACTTCTCTCCTGGTCA C C CTGAGCCG C CAGTATCTACACA AATTTCTAAGC	1452
QY		1573	ACCGCTCAAGCTATCTGCTTGCTGATCAGCCA AAGCCTGTGAAGGAATCAAGTATCCT	1632
Db		1453	ACCGCTCAAGCTATCTGCTTGCTGATCAGCCA AAGCCTGTGAAGGAATCAAGTATCCT	1512

QY 1633 GAGAAATTGCCAGAGAAATTATATGATGCAAAACACAGTGCAGGTGGCAGTTCCGAGAG 1692
DB 1513 GAGAAATTGCCAGAGAAATTATATGATGCAAAACACAGTGCAGGTGGCAGTTCCGAGAG 1572
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DB 1633 CGTATTGGAAGAAATGTGAGACTAAATTATATGCGCAGCAGAGAGGCAAAATTTGTGGG 1692
QY 1813 CATGACATGTGTGCCCGGGGAGAGCAGTGTGTGAATATGTGTGTAAGGCCCAAGCCC 1872
DB 1693 CATGACATGTGTGCCCGGGGAGAGCAGTGTGTGAATATGTGTGTAAGGCCCAAGCCC 1752
QY 1873 ACCCATGGCCACTGGTCCGGAAGTGTCTTCTTGGTCCCATGCTCCAGAGCCTGCGAGGG 1932
DB 1753 ACCCATGGCCACTGGTCCGGAAGTGTCTTCTTGGTCCCATGCTCCAGAGCCTGCGAGGG 1812
QY 1933 GGAGTATCTCATAGAGAGTGCCTCTGCAACCAACCCCAAGCCATGCGATGAGGGAAAGTTT 1992
DB 1813 GGAGTATCTCATAGAGAGTGCCTCTGCAACCAACCCCAAGCCATGCGATGAGGGAAAGTTT 1872
QY 1993 TGTGAGGGCTCCACTGCGACTGTGAAGCTCTGCAACAGTCAGAAATGTCCCGGGAGCAGT 2052
DB 1873 TGTGAGGGCTCCACTGCGACTGTGAAGCTCTGCAACAGTCAGAAATGTCCCGGGAGCAGT 1932
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DB 1933 GTTGACTTCCGTGCTGCTCAGTGTGCCGAGCAACAGCAGACGATTCAAGGGCGGCAC 1992
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DB 1993 TACAAGTGAAGCCTTACACTCAAGTAGAAGATCAGAGCTTAATGCAAACTTAATCTGTATC 2052
QY 2173 GCAGAAGGATTTGATTTCTTCTTTTCTTGTGCAAAATAAAGTCAAAAGTGGACTCCATGC 2232
DB 2053 GCAGAAGGATTTGATTTCTTCTTTTCTTGTGCAAAATAAAGTCAAAAGTGGACTCCATGC 2112
QY 2233 TCGGAGGATAGCCGTAATGTTGTATAGATGGGATATGTGAGAGAGTTGATGTGACAAAT 2292
DB 2113 TCGGAGGATAGCCGTAATGTTGTATAGATGGGATATGTGAGAGAGTTGATGTGACAAAT 2172
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DB 2233 TGCACGATTCACAGGGGTCTCTACACCAAGCACACACACCAACAGTATTAATCACATG 2292
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DB 2293 GTACACCATCTCTTCTGAGCCCGGAGTATCCGATCTATGAAATGAACGTCCTACCTCC 2352
QY 2473 TACATTTCTGTGCGCAATGCCCTCAGAAGGTAATACTGAATGGGCACTGGACCGTGAC 2532
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DB 2473 CCCGAGAACTTAATCGCTACTGGAACCAACCAAGAGACATGATTGTGAGCTGCTGTTT 2532
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DB 2593 CAGCCCCCTGCCAGCCAGCTACACTTGGGCCATCGTCGCTGTGAGTGTCCGTGTCC 2652
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DB 2653 TGCCGAGGGGG 2663

RESULT 3
US-09-930-872-5
; Sequence 5, Application US/09930872
; Patent No. 6448388
; GENERAL INFORMATION:
; APPLICANT: Fridde, Carl Johan
; APPLICANT: Hilbun, Erlin
; TITLE OF INVENTION: No. 6448388el Human Proteases and Polynucleotides Encoding the San
; FILE REFERENCE: LEX-0219-USA
; CURRENT APPLICATION NUMBER: US/09/930, 872
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225, 852
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4042
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-930-872-5
Query Match 64.8%; Score 1874.6; DB 3; Length 4042;
Best Local Similarity 84.4%; Pred. No. 0;
Matches 2287; Conservative 0; Mismatches 179; Indels 245; Gaps 6;
QY 202 GCAGGCACTGCGTGGCCATGGGACCCGCAAGCGGCGCCTGGAGCCCGAGCGTCCC 261
DB 167 GCAGGCACTGCGTGGCCATGGGACCCGCAAGCGGCGCCTGGAGCCCGAGCGTCCC 226
QY 262 GCGTCTCTCCACCCCGGAGCGCGCGGCTGGATGAAAAGGCGGACATGATGAA 321
DB 227 GCGTCTCTCCACCCCGGAGCGCGCGGCTGGATGAAAAGGCGG----- 273
QY 322 GCTGAAACCATGTTCTCAACAACTAACAAGAAACAGAAAACCAACTGATGTT 381
DB 274 ----- 273
QY 382 CTCACCTAATATGACCTGTGTCTTCCCTACGAGGTTGACCAAGGGGCGATTACGTGTCC 441
DB 274 -----AATATGACCTGTGTCTTCCCTACGAGGTTGACCAAGGGGCGATTACGTGTCC 326
QY 442 CATGAATCATGACCATCAAGCGGCGGAGAAAGACGAGTGGCCGTGTCCGAGGTTGAGTCT 501
DB 327 CATGAATCATGACCATCAAGCGGCGGAGAAAGACGAGTGGCCGTGTCCGAGGTTGAGTCT 386
QY 502 CTTACCTTGGGCTGAAAAGGCCCGGACGACTTCCACATGATCTGAGGACTTCCAGC 561
DB 387 CTTACCTTGGGCTGAAAAGGCTCCAGGACGACTTCCACATGATCTGAGGACTTCCAGC 446
QY 562 AGCTAGTGGCTCTGGCTTATTGTGACAGACGTTGGGAAAGACAGGCACTAAGTCTGTG 621
DB 447 AGCTAGTGGCTCTGGCTTATTGTGACAGACGTTGGGAAAGACAGGCACTAAGTCTGTG 506
QY 622 CAGACTTTACCGCAGAGGACTTCTGTTTCTATCAAGGCTCTTGGCATCACAGAAAC 681
DB 507 CAGACTTTACCGCAGAGGACTTCTGTTTCTATCAAGGCTCTTGGCATCACAGAAAC 566
QY 682 TCGGCATTCGATGAGGGAAAGTTCTGTGAGGGCTCCACTCGCACTGAAAGCTGTGCAAC 741
DB 567 TCCTCA-----GTGGCCCTTCAACCTGCCAAGGCTGTGCA 602
QY 742 AGTCAGAAATGTCCCGGAGCAGTGTGACTTCCGTGCTGCTCAGTGTGCCGAGCACAAC 801
DB 603 GGCATGATACGAACAGAGAGGACAGATTACTTCTTAAGGCCAATTCTTACACACTCTCA 662

QY 802 AGCAGCGATTTCAGAGGGCGGCTACAAGTGG--AAGCCTTACACTCAAGTAGAAGCCG 859
Db 663 TGGAAACTCGGAGAGCTGCCCAAGGAGCTCGCCATCCACGTACTGTACAGAGATCC 722
QY 860 ACTTATGCAAACTCTACTGTATGCGAGAAGATTTGATTTCTTTCTTTGTCAATA 919
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QY 920 AAGTCAAGATGGGACTCCATGCTCGAGGATAGCCGTAATGTTTGTATAGATGGGATAT 979
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QY 980 GTGAGCTCAGTGTGTGTCCACACTGTC-GCAGATGCCCCAGCCTCCCAAGAGAAGCTC 1038
Db 831 AAGCAGCATTTCTGTGGAAGACGCAAGAAATACATGCCCAAGCCTCCCAAGAGAAGCTC 890
QY 1039 TTCATCTTGCCAGATGAGTATAAGTCTTGCTTAAGGATAGCGCTCTCTTGAGGTCC 1098
Db 891 TTCATCTTGCCAGATGAGTATAAGTCTTGCTTAAGGATAGCGCTCTCTTGAGGTCC 950
QY 1099 CATAGAAATGAAGAACTGAACGTTGAGACCTTGGTGTGTGCGACAAAAGATGATGCAA 1158
Db 951 CATAGAAATGAAGAACTGAACGTTGAGACCTTGGTGTGTGCGACAAAAGATGATGCAA 1010
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Db 1071 TTATTCAAGAATGGAACAATAGAGGAAACATCAATTGCAATTGTAGTCTGATTCTT 1130
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QY 1230 -----TGGATTGATGGGGAAGATGGGACTGTCTATGACCAAGCCCATC 1272
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Db 1311 GCAACCCATAAGTGAATGTGTAAATATCGCAGCTGCACGATTTAATGAAGATACAGGT 1370
QY 1393 CTTGGACTGGCCTTCAACCATGGCCATGAGTCTGGAACAACATTTGGCATGATTCATGAT 1452
Db 1371 CTTGGACTGGCCTTCAACCATGGCCATGAGTCTGGAACAACATTTGGCATGATTCATGAT 1430
QY 1453 GGAGAAGGGAACTGTGTAAAAAGTCCGAGGGCAACATCATGTCCCTACATTTGGCAGGA 1512
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Db 1851 ACCCATGGCCACTGTGCGACTGTGTTCTTGTGTTCCCATGCTCCAGGACCTGCGGAGGG 1910
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Db 1911 GGAGTATCTATAGAGTGCCTCTGCAACCAACCCCAAGCCATGCGATGAGGGAAGTTC 1970
QY 1993 TGTAGGGCTTCACCTGCACTCTGAAGCTCTGCAACAGTCAGAAATGTCCCGGGACAGT 2052
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QY 2593 CCCGAGACTTAATCGCTACTGGAACCAACCAAGAGACATGATTGTGAGCTGTGTT 2652
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Db 2751 TCGGAGGGGG 2761

US-10-217-774-5
; Sequence 5, Application US/10217774
; Patent No. 6734007
; GENERAL INFORMATION:
; APPLICANT: Fridde, Carl Johan
; APPLICANT: Hilbun, Erin
; TITLE OF INVENTION: No. 6734007e1 Human Proteases and Polynucleotides Encoding the
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0219-USA
; CURRENT APPLICATION NUMBER: US/10/217,774
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US/09/930,872
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,852
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4042
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-217-774-5

Query Match 64.8%; Score 1874.6; DB 4; Length 4042;
Best Local Similarity 84.4%; Pred. No. 0;
Matches 2287; Conservative 0; Mismatches 179; Indels 245; Gaps 6;

QY 202 GCAGGACCTGCGTGGCCCATGGGACCCGCGGAGGAGCCGCTGGGAGCCCGACGCTCC 261
DB 167 GCAGGACCTGCGTGGCCCATGGGACCCGCGGAGGAGCCGCTGGGAGCCCGACGCTCC 226
QY 262 GCGTCCTCTCCACCCGCGGAGCGGCGGCTGGATGGAAGGCGGACATGATGAA 321
DB 227 GCGTCCTCTCCACCCGCGGAGCGGCGGCTGGATGGAAGGCGG----- 273
QY 322 GCTGGAACCATCGTCTCAGCAACTAACAGGAACAGAAACCAACACTGCATGTT 381
DB 274 ----- 273
QY 382 CTCACCTCAATATGACCTGCTCTGCTTACGAGGTTGACCAAGGGCGATTACGTCTC 441
DB 274 -----AATATGACCTGCTCTGCTTACGAGGTTGACCAAGGGCGATTACGTCTC 326
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QY 502 CTTCAACCTTGGGCTGAAAAGGCCCCAGGACGACTTCCACATGATCTGAGACTTCCAGC 561
DB 387 CTTCAACCTTGGGCTGAAAAGGCTCCAGGACGACTTCCACGATGATCTGAGACTTCCAGC 446
QY 562 AGCCTAGTGGCTCTGCTTTATTTGTGCAAGCGTTGGAAAGACAGGACACTAAGTCTGTG 621
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DB 1371 CTTGACTGGCCTTCAACATTGCCCCATGAGTCTGACACAACTTTGGCATGATTCATGAT 1430
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QY 1813 CATGACATGTGTGTGCGGGGAGAGACAGTGTGAATAATGTGTATGAAGGCCCAAGCCC 1872
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QY 1993 TGTGAGGGCTCCACTGCGACTCTGAAAGCTCTGCAACAGTCAGAAATGTCCCCGGGACAGT 2052
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QY 2293 GTCTTGGATCTGATGCTGTTGAAGAGCTGTGCGGGGTGTGTAACGGGAATAACTCAGCC 2352
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DB 2331 TGCACGATTCAAGGGGTCTCTACACCAAGACCAACACCAACCAAGTATATCAATG 2390
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DB 2391 GTCAACATTCCTTCTGAGAGCCCGAGTATCCGCACTTATGAAATGAACGTCTTACTCC 2450
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DB 2451 TACATTTCTGTGCGCAATGCCCTCAGAAAGTACTACTGAATGGGCACTGACCGTGAC 2510
QY 2533 TGGCCCGGCGGTACAATTTTGGGGCACTACTTTCGACTACAGACGGTCTTAAATGAG 2592
DB 2511 TGGCCCGGCGGTACAATTTTGGGGCACTACTTTCGACTACAGACGGTCTTAAATGAG 2570
QY 2593 CCCGAGAATTAACTGCTACTGGAACAACCAAGACACACTGATTTGTGAGCTGCTTT 2652
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DB 2751 TCGCGAGGGGG 2761

RESULT 5
US-09-930-872-1
; Sequence 1, Application US/09930872
; Patent No. 6448388
; GENERAL INFORMATION:
; APPLICANT: Fridde, Carl Johan
; APPLICANT: Hilbun, Erln

; TITLE OF INVENTION: No. 6448388e1 Human Proteases and Polynucleotides Encoding the San
; FILE REFERENCE: LEX-0219-USA
; CURRENT APPLICATION NUMBER: US/09/930,872
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,852
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1476
; TYPE: DNA
; ORGANISM: homo sapiens
; US-09-930-872-1

Query Match 22.9%; Score 663; DB 3; Length 1476;
Best Local Similarity 71.5%; Pred. No. 2.5e-183;
Matches 1079; Conservative 0; Mismatches 185; Indels 245; Gaps 6;
QY 202 GCAGGACCTGGCTGGCCATGGGACCCGACGGGACGGCTGGAGCCCGAGCTGCC 261
DB 69 GAGGACCTGGCTGGCCATGGGACCCGACGGGACGGCTGGAGCCCGAGCTGCC 128
QY 262 GCGTCTCTCTCCACCCCGGAGCGGGCTGGATGGAAGGCGGACATGATGA 321
DB 129 GCGTCTCTCTCCACCCCGGAGCGGGCTGGATGGAAGGCGGCGGCTGGATGGAAGGCGG 175
QY 322 GCTGGAACCATCTCTCTCAGCAACTAACAGGAACAGAAACCAACACTGCATGTT 381
DB 176 ----- 175
QY 382 CTCACCTAATATGACCTGTGCTCTGCTTACGAGGTTGACCAAGGGCGATTACGTGCC 441
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QY 442 CATGAATCATGCAACCATCAGCGGGGAGAGAGACAGTGGCGGTGTCCGAGTTGAGTCT 501
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DB 289 CTTACCTTGGGCTGAAAGGCGGACGACGACTTCCACATGATCTGAGGACTTCCAGC 348
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QY 622 CAGACTTTACCGCCAGAGGACTTCTGTTTATCAAGGCTTTTGCATCACAAGAAAC 681
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QY 682 TCGCCATCGCATGGAAGGAAAGTTCTGTGAGGCTCCACTCGCACTGTGAAGCTCTGCAAC 741
DB 469 TCCTCAGTGG-----CCCTTCAACCTGCCAAGGCTTGTCA 504
QY 742 AGTCAGAAATGTCCCGGACAGTGTGACTTCCGTGCTGCTGAGTGTCCGAGCACAAC 801
DB 505 GGCATGATAGCAAGAGAGGAGATTACTTCTTAAGGCCACTTCTTCAACACTCTCA 564
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DB 625 ACAGAGCCCATGCTCTCGGGGACAGTGAAGTCTGTGACCTC-----AAGG 672
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QY 1219 TTATTCAAAGA----- 1229
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QY 1230 ----- 1229
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QY 1393 CTTGGACTGGCTTCAACCATTCGCCATGAGTCTGGACACAACTTTGGCATGATTCATGAT 1452
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QY 1453 GGAGAAGGGAACATGTGTAAAGTCCGAGGGCAACATCATGTCCCTACTATGGCAGGA 1512
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Db 1333 GGAGAAGGGAACATGTGTAAAGTCCGAGGGCAACATCATGTCCCTACTATGGCAGGA 1392
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QY 1513 CGCAATGAGTCTTCTCTGTGTCACCTGCGAGCCGCCAGTATCTACACAAATTTCTAAGC 1572
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Db 1393 CGCAATGAGTCTTCTCTGTGTCACCTGCGAGCCGCCAGTATCTACACAAATTTCTAAGA 1452
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QY 1573 ACCGCTCAA 1581
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Db 1453 TCAGTGAAA 1461
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RESULT 6
US-10-217-774-1
; Sequence 1, Application us/10217774
; Patent No. 6734007
; GENERAL INFORMATION:
; APPLICANT: Fridde, Carl Johan
; APPLICANT: Hilbun, Erin
; TITLE OF INVENTION: No. 6734007e1 Human Proteases and Polynucleotides Encoding the
; FILE OF INVENTION: Same
; FILE REFERENCE: LEX-0219-USA
; CURRENT APPLICATION NUMBER: US/10/217,774
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US/09/930,872
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,852
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1476
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-217-774-1
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Query Match 22.9%; Score 663; DB 4; Length 1476;
Best Local Similarity 71.5%; Pred. No. 2.5e-183;
Matches 1079; Conservative 0; Mismatches 185; Indels 245; Gaps 6;

QY 202 GCAGGACCTGCGTCCGATGGGATGGGACCCGACAGCGGCGCTGGAGCCCGAGCGTCCC 261
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Db 69 GCAGGACCTGCGTCCGATGGGATGGGACCCGACAGCGGCGCTGGAGCCCGAGCGTCCC 128
|||||
QY 262 GCGTCTCTCCACCCCGGAGCGGCGCGCTGGATGGAAGGCGGGACATGATGAA 321
|||||
Db 129 GCGTCTCTCCACCCCGGAGCGGCGCGCTGGATGGAAGGCGGGACATGATGAA 175
|||||
QY 322 GCTGAAACCATCGTTCTCAGCAAACTAACAGGAAGAAAAACCAACACTGCATGTT 381
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Db 176 ----- 175
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QY 382 CTCACATATATGACCTGCTCTGCTTACGAGTTGACCAAGGGCGATTAAGTGTCC 441
|||||
Db 176 -----AATATGACCTGCTCTGCTTACGAGTTGACCAAGGGCGATTAAGTGTCC 228
|||||
QY 442 CATGAATCATGCAACCATCAGCGGCGGAGAAAGAGCAGTGGCCGTGCCGAGTTGAGTCT 501
|||||
Db 229 CATGAATCATGCAACCATCAGCGGCGGAGAAAGAGCAGTGGCCGTGCCGAGTTGAGTCT 288
|||||
QY 502 CTTACCTTCGGCTGAAAGGCGGCGGAGCAAGCTTCCACATGATCTGAGGACTTCCAGC 561
|||||
Db 289 CTTACCTTCGGCTGAAAGGCGTCCAGGCAAGCTTCCAGTGGATCTGAGGACTTCCAGC 348
|||||
QY 562 AGCTTAGTGGCTCCTGGCTTATGTGAGAGAGCTTGGGAAAGAGCAAGGCACTAAGTCTGTG 621
|||||
Db 349 AGCTTAGTGGCTCCTGGCTTATGTGAGAGAGCTTGGGAAAGAGCAAGGCACTAAGTCTGTG 408
|||||
QY 622 CAGACTTTACCGCCAGAGGACTTGTGTTCTATCAAGGCTTTGGCATCACACAGAAAC 681
|||||
Db 409 CAGACTTTACCGCCAGAGGACTTGTGTTCTATCAAGGCTTTGGCATCACACAGAAAC 468
|||||
QY 682 TCGCCATCGCATGAGGGAAGTCTGTGAGGGCTCCACTCGCACTCTGAAGCTCTGCAAC 741
|||||
Db 469 TCCTCAGTG-----CCCTTTCAAACCTGCCAAGGCTGTGTCA 504
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QY 742 AGTCAGAAATGTCCCGGGAAGAGTGTGACTTCCGTGCTCAAGTGTGCCAGACAAAC 801
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Db 505 GGCATGATACGAACAGAAAGAGGAGATTACTTCTTAAGGCCACTTCTTACACACCTGTCA 564
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QY 802 AGCAGAGATTCAAGGGCGGCACTACAGTGG--AAGCTTACACTCAAGTAGAAGCCG 859
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Db 565 TGAAGCTCGGCAAGAGCTGCCCAAGGCAAGCTCGCCATGCCAGTACTGTACAAAGAGATCC 624
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QY 860 ACTTATGCAAACTCTACTGTATCGCAGAAAGATTGATTTCTTTCTTTGTCAAATA 919
|||||
Db 625 ACAGAGCCCATAGTCTCTGGGGCCAGTGAAGTCTGTGACCTC-----AAGG 672
|||||
QY 920 AAGTCAAGATGGGACTTCATGCTCGAGAGATAGCCGTAATGTTGTATAGATGGATAT 979
|||||
Db 673 ACATGGAGCTGGCAGATCAACCCCTGCAACAGCAGCAGCTTGGCTGGGACTGCCACAA 732
|||||
QY 980 GTGAGCTCAGTGTGTCTCCACATCTGCGC-ACATGCCCCAGCGCTCCCAAGGAAGACCTC 1038
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Db 733 AAGCAGATTCTGTGGAAGACGCAAGAAATACATGCCCTCCCAAGGAAGACCTC 792
|||||
QY 1039 TTCACTTTGCCAGATGATTAAGTCTTCTTACCGGATTAAGCGCTCTTCTGAGGTCC 1098
|||||
Db 793 TTCACTTTGCCAGATGATTAAGTCTTCTTACCGGATTAAGCGCTCTTCTGAGGTCC 852
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QY 1099 CATAGAAATGAAGAACTGAACGTGAGAGACCTTGGTGGTGGTCCACAAAAGATGATGCAA 1158
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Db 853 CATAGAAATGAAGAACTGAACGTGAGAGACCTTGGTGGTGGTCCACAAAAGATGATGCAA 912
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QY 1159 AACCATGGCCATGAAAATATCAACCACTACGTGCTCAGATACCTCAACATGTTATCTGCT 1218
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Db 913 AACCATGGCCATGAAAATATCAACCACTACGTGCTCAGATACCTCAACATGTTATCTGCT 972
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QY 1219 TTATTCAAGA----- 1229
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Db 973 TTATTCAAGAATGGAACAATAGAGGAACATCAATTGCAATTGTAGTCTGATTCTT 1032
QY 1230 ----- 1229
Db 1033 CTAGAAGATGAACAGCCAGAGCTGGTGATAAGTCACACGAGACCAACCTTAAGTAGC 1092
QY 1230 -----TGGATTGATGGGGGAAAGATGGGACTCGTTCATGACCAAGCCCATC 1272
| | | | | | | | | |
Db 1093 TTCTGCCAGTGGCAGTCTGGATTGTGGGAAAGATGGGACTCGTTCATGACCAAGCCCATC 1152
QY 1273 TTACTGACTGTCGTGATATATGTTCCTGGAAGATGAGCCCTGTGACACTTTGGGATTT 1332
| | | | | | | | | |
Db 1153 TTACTGACTGTCGTGATATATGTTCCTGGAAGATGAGCCCTGTGACACTTTGGGATTT 1212
QY 1333 GCACCCATAAGTGAATGTGTAGTAAATATCGCAGCTGCACGATTAAAGAATACAGGT 1392
| | | | | | | | | |
Db 1213 GCACCCATAAGTGAATGTGTAGTAAATATCGCAGCTGCACGATTAAAGAATACAGGT 1272
QY 1393 CTGGAGCTGGCCTTCACCATTTGCCATGAGTCTGGACACAACTTTGGCATGATTCATGAT 1452
| | | | | | | | | |
Db 1273 CTGGAGCTGGCCTTCACCATTTGCCATGAGTCTGGACACAACTTTGGCATGATTCATGAT 1332
QY 1453 GGAGAAAGGGAACATGTGTAAAAAGTCCGAGGGCAACATCATGTCCCTTACATTGGCAGGA 1512
| | | | | | | | | |
Db 1333 GGAGAAAGGGAACATGTGTAAAAAGTCCGAGGGCAACATCATGTCCCTTACATTGGCAGGA 1392
QY 1513 CGCAATGAGTCTTCTCTCTGCTGTCACCCCTGCAGCGCCCATGATCTACACAAATTTCTAAGC 1572
| | | | | | | | | |
Db 1393 CGCAATGAGTCTTCTCTCTGCTGTCACCCCTGCAGCGCCCATGATCTACACAAATTTCTAAGA 1452
QY 1573 ACCGCTCAA 1581
| | | |
Db 1453 TCAGTGAAA 1461

RESULT 7
US-09-963-791-23
; Sequence 23, Application US/09963791
; Patent No. 6649399
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Scoville, John
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6649399e1 Human Proteases and Polynucleotides Encoding the Sa
; FILE REFERENCE: LEX-0105-USA
; CURRENT APPLICATION NUMBER: US/09/963,791
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 60/169,769
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 2274
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-963-791-23

Query Match 7.8%; Score 227; DB 4; Length 2274;
Best Local Similarity 50.1%; Pred. No. 1.6e-55;
Matches 721; Conservative 0; Mismatches 685; Indels 33; Gaps 5;

QY 1253 CTGTCATGACCAAGCCATCTTACTGACTGTCGTGATATATGTTCTGGAAGATGAGC 1312
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Db 590 CCCACCAAGATATGCAATTCTTATTAAGATATGATATCTGCACTTATAAAAATAAGC 649
QY 1313 CCTGTGACACTTTGGGATTTGACCAATGAGTGAATGTGTAGTAAATATCGCAGCTGCA 1372
| | | | | | | | | |
Db 650 CCTGTGGAACACTGGGCTTGGCTCTGTGCTGGAATGTGTGAGCCTGAAAAGAGCTGCA 709

QY 1373 CGATTAATGAAGATACAGGTCTTGGACTGGCCTTCACCAATTGCCCATGAGTCTGGACACA 1432
| | | | | | | | | |
Db 710 GCATTAATGAAGACATTTGGCCTGGGTTGAGCTTTTACCATTTGACATGAGATTGGTCACA 769
QY 1433 ACTTGGCATGATTCATGATGGAAGGGAACATGTGTAAA-----AGTCCGAGG 1483
| | | | | | | | | |
Db 770 ATTTGGTATGAACCATGATGGAATTGGAATTTCTGTGGACGAAAGGTCAATGAAGCAG 829
QY 1484 GCAACATCATGTCCCTACATTTGGCAGGACGCAATGAGTCTTCTCTGCTGTCACCTGCA 1543
| | | | | | | | | |
Db 830 CAAAATTATGCAAGCTCACAATTTACTGCGAATCAATCTTTTCTGCTGCTGCA 889
QY 1544 GCCGCCAGTATCTACAAATTTCTAAGCACGCTCAAGCTATCTGCTTGTGATCAGC 1603
| | | | | | | | | |
Db 890 GTGAGACTTACATCACAGCTTTCTGATTCAGGCCGTGTACTTGCTTGTATATGAGC 949
QY 1604 CAAAGCCTGTGAAGGAATACAGTATCTGAGAAATTGCCAGAGAAATTATATGATGCAA 1663
| | | | | | | | | |
Db 950 CT---CCCAAGCGTGAATTTCTTTATCCAGCTGTGCCCCCAGGTCAAGTGTATGATGCTG 1006
QY 1664 ACACACAGTGAAGTGGCAGTTCGAGAGAAAGCCAAAGCTCTGATGCTGCACTTAAAA 1723
| | | | | | | | | |
Db 1007 ATGAGCAATGTCTTTCCAGTATGGAAGCAACTCCCGCAATGTAAATATG----- 1057
QY 1724 AGCAGTCTGTAAAGCCCTGTGCTCCATCTGTAATGGAAGAAATGTGAGACTAAATTTA 1783
| | | | | | | | | |
Db 1058 GGGAAAGTGTGAGAGCTCTGTGTCTCAGCAAAAGCAACCGCTGTGTACCAACAGTA 1117
QY 1784 TGCCAGCAGAGAAAGCACAAATTGTGGGACATGATGTGTCGGGAGGAGCAGTGTG 1843
| | | | | | | | | |
Db 1118 TTCCAGCAGCTGAGGGGACACTGTGTCAAACTGGGAATATTGAAAAAGGTGTATTATC 1177
QY 1844 TGAATATGATGAT-----GAAAGCCCCAAGCCCAAGCCCATGGCCACTGTGCGACT 1894
| | | | | | | | | |
Db 1178 AGGAGATTTGTCTCTTTGGCACTTGGCCCCAGACATAGATGGGGGTGCTCCCT 1237
QY 1895 GGTCTTCTTGGTCCCATGCTCCAGGACCTGGGAGGGGAGTATCTCATAGAGTCCGCC 1954
| | | | | | | | | |
Db 1238 GGTCACTATGGGAGAGTGCAGCAGACCTGGGGGAGGCGTCTCTCATCCCTAAGAC 1297
QY 1955 TCTGCACCAACCCCAAGCCATCGCATGAGGGAAGTCTGTGAGGGCTCCACTCGCACTC 2014
| | | | | | | | | |
Db 1298 ACTGTGACAGTCCAGCACCTTCAGGAGGTGGAATAATTGCTTGGGAAAGAAACGCT 1357
QY 2015 TGAAGCTGTGCAACAGTCAGAAATGTCCCGGGACAGTGTGACTTCCGTGCTCAGT 2074
| | | | | | | | | |
Db 1358 ATCGCTCCTGTAAACAGATTCATGCCCTTTGGGTTCCCGAATTTTGAAGAAACAGT 1417
QY 2075 GTGCCGAGCACAACAGCAGATTCAGAGGGGCGCACTACAAGTGAAGCCTTACACTC 2134
| | | | | | | | | |
Db 1418 GTGCAGACTTTGAACATATGCTTTCCGAGGAAAGTATTATTAACGTGAACCTTACT- 1476
QY 2135 AAGTAGAAGATCAGGACTTATGCAAACTCTACTGTATCGCAGAAAGATTGATTTCTTCT 2194
| | | | | | | | | |
Db 1477 --GAGGTGGGTAACCTTGTGCATTAACCTGCTTGGCTGAAGTTATATTCTACA 1534
QY 2195 TTTCTTTGTCAAAATAAGTCAAAAGATGGGACTTCATGCTCGAGAGATAGCCGTAATGTT 2254
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Db 1535 CTGAACGTGCTCTCGGCTGATCGATGGGACCAAGTGCAATGGGATTCACCTGATATCT 1594
QY 2255 GTATAGATGGGATATGTGAGAGAGTTGATGTGCAATGTCTTGGATCTGATGCTGTTG 2314
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Db 1595 GCATCAATGGAATGCAAGCAGTAGGCTGTGATTAATTTGGGATCTGATGCTTAGGG 1654
QY 2315 AAGACGTCTGTGGGGTGTGTAAACGGGAATACTCAGCCTGCACGATTACAGGGGCTCT 2374
| | | | | | | | | |
Db 1655 AAGATGATGTGAGTCTGTGAGGGGACGGAAGCACATGTGATGCCATTGAAGGTTCT 1714
QY 2375 ACACCAAGCACCACACACCAACCAAGTATTATCAATGTGTCAACATTCTTCTGAGCCC 2434
| | | | | | | | | |
Db 1715 TCAATGATTCTGCCCCAGGGGAGGCTACATGGAAGTGTGTGAGATTAACCAAGAGCTCTG 1774

QY 2435 GGAGTATCCGCATCTATGAAATGAAAGTCTTACCTCTACATTTCTGTGCGCATGCC 2494
DB 1775 TTCACATTGAAGTTAGAGAAAGTTGCCATGTCAAGAACTATATGTCTTAAAACTGMAAG 1834
QY 2495 TCAGAAAGTACTACTGTAATGGGCACTGACCCGTGACTGGCCCGGCGGTACAAATTTT 2554
DB 1835 GAGATGATTACTATATTAATGGTGCCTGGACTATGACTGGCTTAGAAATTTGATGTTG 1894
QY 2555 CGGGCACTACTTTTGCAGTACAGACGGTCTCTATTAAGAGCCCGAAGCTTAATCGCTACTG 2614
DB 1895 CTGGGACAGCTTTTCAATTACAGAGAACCAACTGATGAACAGAAATCTTGAAAGCTCTAG 1954
QY 2615 GACCAACCAACGAGACACTGATGTGGAGCTGTCTTCAAGGAGAAACCGGGTGT 2673
DB 1955 GTCTTACCTCAGAAAATCTCATCGTCTATGTCTTCTTCAAGAACAGAAATTTGGGAATT 2013

RESULT 8

US-09-963-791-1
; Sequence 1, Application US/09963791
; Patent No. 6649399
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Scoville, John
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Archur T.
; TITLE OF INVENTION: No. 6649399e1 Human Proteases and Polynucleotides Encoding the SA
; FILE REFERENCE: LEX-0105-USA
; CURRENT APPLICATION NUMBER: US/09/963,791
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 60/169,769
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2727
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-963-791-1

Query Match 7.8%; Score 227; DB 4; Length 2727;
Best Local Similarity 50.1%; Pred. No. 1.7e-55;
Matches 721; Conservative 0; Mismatches 685; Indels 33; Gaps 5;

QY 1253 CTCGTCATGACCAAGCCATCTTAAGTCTGCTGTGATATATGTTCTCGAAGATGAGC 1312
DB 1043 CCCACCACGATTAATGAGTCTTATTAATGATATGATATCTGCACTTATTAATAAGC 1102
QY 1313 CCTGTGACACTTTGGATTGGCAACCATTAAGTGAATGTAGTAATATGCGAGCTGCA 1372
DB 1103 CCTGTGAACACTGGGCTTGCTCTGTGCTGGAATGTGAGCCTGAAGAGAGCTGCA 1162
QY 1373 CGATTATGAAGATACAGTCTTGAGCTGCTTCAACATGCCCAGTGAAGTCTGAGACA 1432
DB 1163 GCATTATGAAGACATTGGCTGGGTTCAGCTTTTACCATGACATGAGATTGCTACA 1222
QY 1433 ACTTTGCGATGATTCATGATGAGAGGAACATGTGTAAAA-----AGTCCGAGG 1483
DB 1223 ATTTTGTATGAACCATGATGGAATTTGGAATTTCTGTGGAGCAAGGTCATGAAGCAG 1282
QY 1484 GCAACATCATGTCCCTACATTTGGCAGACGAATGAGTCTTCTCTGTCACCCCTGCA 1543
DB 1283 CAAAACTTATGGCAGCTCACTACTGCAATACCAATCCTTTTCTGCTGCTGCA 1342
QY 1544 GCCGCACTATCTACAAATTTCTAAGCACCGCTCAAGCTATCTGCTTCTGATCAGC 1603
DB 1343 GTCGAGACTACATCACCAAGCTTTCTAGATTGAGGCCGTGTAATTGCTTGAATGAGC 1402
QY 1604 CAAAGCTGTGAAGAAATACAGTATCCTGAGAAATGCGCAGAGAAATATATGATGCA 1663
DB 1403 CT---CCCAAGCGTGAAGTCTTCTTATCTCAGCTGTGCCCCAGGTCAAGGTATGATGCTG 1459

QY 1664 ACACACAGTCAAGTGGCAGTTCGGAGAGAAAGCCAAAGCTCTGCATGCTGCACTTTAAA 1723
DB 1460 ATGAGCAATGTCTGTTTCCAGTATGAGAGCAACCTCCCGCAATGTAAATATG----- 1510
QY 1724 AGGACATCTGTAAGCCCTGTGTGTCATCGTATTTGGAAGAAATGTGAGACTAATTTTA 1783
DB 1511 GGAAGTGTGTAAGAGCTCTGTGTCTCAGCAAAAAGCAACCGCTGTGTCAACCAAGTA 1570
QY 1784 TGCCAGCAGCAGAGGCAATTTGTGGCATGACATGTGTGTCGGGGAGGAGACAGTGTG 1843
DB 1571 TTCCAGCAGCTGAGGGGACACTGTGTCAAACTGGGAATATTGAAAAAGGGTGTGTATC 1630
QY 1844 TGAATATGTGTAT-----GAAGCCCCCAAGCCCAATGCGCCACTGTGCGACT 1894
DB 1631 AGGAGATTTGTGTTCTTTTGGCACTTGCCCCCAGAGCATATGATGGGGCTGGGGTCCCT 1690
QY 1895 GGTCTTTGTGTCCTCCATGCTCCAGAGCTTCCGAGGGGAGATATCTCATAGAGTCCGC 1954
DB 1691 GGTCACTATGGGGAGAGTGCAGCAGAGACTTGGGGGAGGGCTCTCTCATCTCCCTAAGAC 1750
QY 1955 TCTGCACCAACCCCAAGCCATGCGATGGAGGGAAGTTCTGTGAGGGCTCACTCGCACTC 2014
DB 1751 ACTGTGACAGTCCAGCAGCTTTCAGAGAGTGAATAATATGCTTGCGGGAAGAAACCGT 1810
QY 2015 TGAAGCTCTGCAACAGTTCAGAAATGTCTCCCGGACAGTGTGACTTCCGTGCTCAGT 2074
DB 1811 ATGCTCTCTGTAAACAGATCCATGCTCTTTGGGTTCCCGAGATTTTGAGAGAAACAGT 1870
QY 2075 GTGCCGACACAAACAGCAGACGATTTAGAGGGCGGCACTCAAGTGAAGCCTTACACTC 2134
DB 1871 GTGCAAGCTTTGACAAATATGCTTCCGAGGAAAGTATTAATCTGAAACCCTATACT- 1929
QY 2135 AAGTAGAAGATCAGGACTTATGCAAACTCTACTGTATGCGAGAGATTGATTCTTCT 2194
DB 1930 --GGAGGTGGGGTAAACCTTGTGCAATTAACCTGCTGGCTGAAGGTTAATTTCTACA 1987
QY 2195 TTTCTTTGTCAATTAAGTCAAGATGGGACTCCATGCTCGAGAGATAGCCGTATGTTT 2254
DB 1988 CTGAACGCTCTCCTCGGTGATCGATGGGAAACCCAGTCAATGCGGATTCATCGATATCT 2047
QY 2255 GTATAGTGGGATATGAGAGAGTGGATGTGACAAATGTCCTTGATCTGATGCTGTTG 2314
DB 2048 GCATCAATTGGAAGATGCAAGCAGCTGAGCTGTGATTAATTTTGGATCTGATGCTAGG 2107
QY 2315 AAGACGCTGTGGGGTGTGTAACGGGAATTAAGTCAAGCTGCAAGATTCAAGGGGTCTCT 2374
DB 2108 AAGATGATGTGAGTGTGTGAGGGGAGCGAAGACATGTGATGCCATTGAAGGGTCTCT 2167
QY 2375 ACACCAAGCACCAACCAACCAAGTATTAATCATATGATGTCACCATTCCTCTGAGGCC 2434
DB 2168 TCAATGATTTCACTGCCAGGGAGGCTACATGGAAGTGTGAGATACCAAGAGGCTCTG 2227
QY 2435 GGAATATCCGATCTATGAATGAAGCTCTTCACTCTCTCAATTTCTGTGCGCAATGCC 2494
DB 2228 TTCACATTTGAAGTTAGAGAAAGTTGCCATGTCAAGAACTATATTGCTTTAAATCTGAAG 2287
QY 2495 TCAGAAAGTACTACTGAAATGGGCACTGACCGTGAAGTGGCCCGGCGGTACAAATTTT 2554
DB 2288 GAGATGATTTACTATATTAATGTGTGCTGACTATGACTGCTGAGAAATTTGATGTTG 2347
QY 2555 CGGGCACTACTTTGCACTACAGACGGTCTTATATGAGCCCGAAGCTTAATCGCTACTG 2614
DB 2348 CTGGGACAGCTTTTCAATTACAGAGAACCAACTGATGAACAGAAATCTTGAAAGCTTAG 2407
QY 2615 GACCAACCAACGAGACACTGATTTGTGAGAGCTGCTTTCAAGGAGAAACCGGGTGT 2673
DB 2408 GTCTTACCTCAGAAAATCTCATCGTCAATGTTGCTTCAAGAACAGAAATTTGGGAATT 2466

RESULT 9
US-09-799-451-411
; Sequence 411, Application US/09799451

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/ Patent No. 6783969
/ GENERAL INFORMATION:
/ APPLICANT: Tang, Y. Tom
/ APPLICANT: Zhou, Ping
/ APPLICANT: Goodrich, Ryle
/ APPLICANT: Abundi, Vinod
/ APPLICANT: Ren, Feiyan
/ APPLICANT: Zhang, Jie
/ APPLICANT: Xue, Aidong J.
/ APPLICANT: Zhao, Qing A.
/ APPLICANT: Wang, Jian-Rui
/ APPLICANT: Yamazaki, Victoria
/ APPLICANT: Chen, Rui-hong
/ APPLICANT: Wang, Zhiwei
/ APPLICANT: Wang, Yonghong
/ APPLICANT: Wehrman, Tom
/ APPLICANT: Ghosh, Reena
/ APPLICANT: Dymnac, Radoje T.
/ TITLE OF INVENTION: No. 6783969el Nucleic Acids and
/ FILE REFERENCE: Polypeptides
/ CURRENT APPLICATION NUMBER: US/09/799,451
/ CURRENT FILING DATE: 2001-03-05
/ NUMBER OF SEQ ID NOS: 948
/ SOFTWARE: pt_fl_genes Version 2.0
/ SEQ ID NO 411
/ LENGTH: 3571
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (260) .. (3568)
US-09-799-451-411
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Query Match 7.2%; Score 209.6; DB 4; Length 3571;
Best Local Similarity 49.4%; Pred. No. 2.6e-50;
Matches 706; Conservative 0; Mismatches 689; Indels 33; Gaps 5;

QY 1240 GGGAAAGATGGGACTCGTCATGACCAAGCCATCTTAAGTGGTCTGATATATGTTCC 1299
DB 1256 GAGAACGGTGTGGCTAACCATGACACAGAGTGTCTATCACACGCTATGACATCTGCATC 1315
QY 1300 TGGAAAGATGAGCCCTGTGACACTTTGGGATTGGACCCATAAGTGAATGTGTAA 1359
DB 1316 TACAAGAACAAACCTGCGGCACACTAGGCGCTGCGCCGCGTGGCGGAATGTGTAGCGC 1375
QY 1360 TATCGCAGCTGCAGATTAATGAAGATACAGGTCTTGGACTGGCCTTCAACATGCCCCAT 1419
DB 1376 GAGAGAAAGCTGACGGCTCAATGAGGACATTGGCTGCCACAAAGCTTCAACATGCCCCAC 1435
QY 1420 GAGCTGTGACACAACTTTGGCATGATTGATGAGAAAGGAACATGT-----GT 1470
DB 1436 GAGATCGGGCACACATTGCGCATGAACCATGACGGCGTGGMAACAGCTGTGGGCCCGT 1495
QY 1471 AAAAAGTCCGAGGGAACATCATGTCCCTTACATTTGCGAGACGCAATGAGTCTTCTCC 1530
DB 1496 GGTACAGAGCCAGCAAGCTCATGGCTGCCACATTAACATGAAGCAACCCATTGCTG 1555
QY 1531 TGGTCAACCTGACGCGCCAGTATCTACAAATTTCTAAGCACCGCTCAAGCTATCTGC 1590
DB 1556 TGGTCATCTGCAACCGTGAATCATCAACAGCTTTCTAGACTCGGGCGCTGCGGCTCTGC 1615
QY 1591 CTGCTGATCAGCCAAAGCCTGTGAAGGAATACAGTATCTGAAATTTGCCAGAGAA 1650
DB 1616 CTGAACAACCGGCC---CCCGACAGAGGACTTTGTGTACCCGACAGTGGCACCGGCCAA 1672
QY 1651 TTAATATGATGCAAAACACACAGTGAAGTGGCAGTTGCGAGAGAAAGCCAAGCTTGCATG 1710
DB 1673 GCCTACGATGACAGATGAGCAATGCGGCTTTCAGCAATGAGTCAAAATCGCGTCAGTGTAAA 1732
QY 1711 CTGGACTTTAAAAAGACATCTGTAAAGCCCTGTGTGTCATCTGTATTGGAAGAAATGT 1770
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DB 1733 TACG-----GGGAGGTCTGACGCGAGCTGTGTGTCTGAGCAAGACCAACCGGTGC 1783
QY 1771 GAGACTAAATTTATGCCAGACGAGGACACAAATTTGTGG-----CATGACATG 1821
DB 1784 ATCAACCAACAGCATCCCGGCCCGGAGGGCACCGCTGTGCCAGACGACACCATGACAAG 1843
QY 1822 TGGTCCGGGGAGGACAGTGTGTAAATATGTGATGAAGGCCCAAGCCCAACCATGGC 1881
DB 1844 GGGTGGTGTCTACAAACGGGTCTGTGTCTCCCTTTGGGTGCGGCCACAGAGGGTGTGAACGGA 1903
QY 1882 CACTGCTCGAGTGTCTTCTTGTGTCCTCCCATGCTCCAGACCTGCGGAGGGGAGTATCT 1941
DB 1904 GCCTGGGGCCGTGAGCTCCATGGGGCGACTGCAAGCCGAGCCTGTGGCGGCGGTGTCC 1963
QY 1942 CATAGGAGTGGCTCTGACCAACCCCAAGCCATGCGATGAGGGAAGTTCTGTAGGGC 2001
DB 1964 TCTTCTAGTGTCACTGCGACAGCCCAAGCCCAACCATCGGGGCAAGTACTGTCTGGGT 2023
QY 2002 TCACCTGCACTCTGAAGCTCTGCAACAGTCAAGAAATGTCCCGGGACAGTGTGACTTC 2061
DB 2024 GAGAGAAAGCGGACCGCTCTGCAACACCGATGACTGTCCCTGCTCCAGACTTC 2083
QY 2062 CGTGCTGCTCAGTGTGCGGACCAACAGACAGATTCAGAGGGCGGCACTACAGTGG 2121
DB 2084 AGAGAAAGTCAAGTGTCTGAATTTGACAGATCTCTTCCGTGGAAATTTCTCAAGTGG 2143
QY 2122 AAGCCTTACCTCAAGTAGAAGATCAGACTTATGCAAACTTACTGTATCGAGAAAGA 2181
DB 2144 AAAACGTACCGGGGAGGGGCGTGAAGGCC---TGCTGCTCAGCTGCTAGCGGAAAGGC 2200
QY 2182 TTGATTTCTTCTTTCTTGTCAATAAAGTCAAGATGGGACTCCATGCTCGAGAGAT 2241
DB 2201 TTCAACTTCTACACGAGAGGGCGGACGCCGTGTGACGGGACACCTGCGCTCCAGAC 2260
QY 2242 AGCCGTAATGTTGTATAGATGGATATGTGAGAGATGTGACAAATGTCCTTGA 2301
DB 2261 AGGTTGACATTTGCGTCAAGTGGCAATGACAGACAGTGGGCTGCGACCGAGTCTGGGC 2320
QY 2302 TCTGATGCTGTGAAGACGTGTGTGGGTGTAAAGGAAATTAAGTCAAGCTGCAAGATT 2361
DB 2321 TCCGACCTGCGGAGAGACAAAGTGCAGATGTGTGGCGGTGACGGCAGTGCCTCGAGACC 2380
QY 2362 CACAGGGGTCTTACACCAAGCACACACACCAACAGATTAATCATGATGTCACCATT 2421
DB 2381 ATGAGGGGCGTCTTACGCCCAAGCTTCACTGGGGCGGTACGAGGATGTGCTGTGATT 2440
QY 2422 CCTTCTGAGCCCGAGATACCGCATCTATGAATGAAGCTCTCTACCTCTCATATTCT 2481
DB 2441 CCCAAAGGCTCCGTCCACATCTTCACTCAAGATCTGAACCTCTCTCAGTCACTGGCC 2500
QY 2482 GTGCCGATGCCCCAGAAAGTACTACCTGAATGGGCACCTGACCCGTGACCTGCCCCGC 2541
DB 2501 CTGAAGGAGAGACAGAGTCCCTGCTGTGAGGGGCTGCTGGGACCCCCCAGCCCCAC 2560
QY 2542 CGGTACAATTTTCGGGCACTATTGACTACAGACGCTCTTAATGAGCCCGAGAAC 2601
DB 2561 CGTCTGCTCTAGCTGGGACCACTTTCACTGCGACAGGGGCAAGACAGTCTCAGAGC 2620
QY 2602 TTAATGCTACTGGAACCAACGAGACACTGATTGTGAGCTGCTG 2649
DB 2621 CTGGAAGCCCTGGGACCGATTAAATGCAATCTCTCATGCTCATGTGTGCTG 2668
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RESULT 10
US-09-981-953A-3
/ Sequence 3, Application us/09981953A
/ Patent No. 6689599
/ GENERAL INFORMATION:
/ APPLICANT: RACIE, LISA A.
/ APPLICANT: TWINE, NATALIE C.
/ APPLICANT: AGOSTINO, MICHAEL J.
/ APPLICANT: WOLFMAN, NEIL
```

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; APPLICANT: MORRIS, ELISABETH A.
; TITLE OF INVENTION: NOVEL AGGRECANASE MOLECULES
; FILE REFERENCE: 08702.0075-00000
; CURRENT APPLICATION NUMBER: US/09/981,953A
; CURRENT FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/242,317
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3377
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Nucleotide
; OTHER INFORMATION: sequence of the aggrecanase molecule
US-09-981-953A-3
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Query Match      7.1%; Score 206.4; DB 4; Length 3377;
Best Local Similarity 49.3%; Pred. No. 2.1e-49;
Matches 704; Conservative 0; Mismatches 691; Indels 33; Gaps 5;
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QY 1240 GGGAAAGATGGAGCTGTCATGACCAAGCCATCTTACTGAGTGTCTGATATATGTTCC 1299
    |||||
DB 1008 GAGAACGGTGTGGCTAACCATGACACAGCAGTGTCTATCACACGCTATGACATCTGCATC 1067

QY 1300 TGGAAAGATGAGCCCTGTGACACTTTGGATTGGCACCCATAGTGAATGTAGTAAA 1359
    |||||
DB 1068 TACAAGAACAAACCTGCGGACACTAGGCTTGCCCGGTGGCGGAATGTGAGCGC 1127

QY 1360 TATCGCAGCTGACGATTAATGAAGATACAGTCTTGAGTGGCCTTACCATTTGCCAT 1419
    |||||
DB 1128 GAGAGAAGCTGACGCTCAATGAGACATTTGGCTGGCCACAGCGTTCAACCATTTGCCAC 1187

QY 1420 GAGTCTGACACAACTTTGGCATGATTCATGATGAGAAGGGAACATGT-----GT 1470
    |||||
DB 1188 GAGATCGGACACATTTGGCATGAAACCATGACGGCGTGGGAAACAGCTGTGGGGCCCGT 1247

QY 1471 AAAAAGTCCGAGGCAACATCATGTCCCTACATTTGGCAGACGCAATGAGTCTTCTCC 1530
    |||||
DB 1248 GGTACAGACCCAGCCAAAGCTCATGTGCTGCCACATTAACATGAAGCAACCCGTTCTGTG 1307

QY 1531 TGGTACCCCTGACCGCCGCAATCTTACAAATTTCTAAGCACCGCTCAAGCTATCTGC 1590
    |||||
DB 1308 TGGTCATCTGACCGCTGATCATCATCACAGCTTTCTAGACTCGGGGCTCTGCTGC 1367

QY 1591 CTGCTGATCAGCCAAAGCCTGTGAAGGAATACAAGTATCTGAGAAATTTGCCAGAGAA 1650
    |||||
DB 1368 CT---GAACAACCGACCCCGGACAGAGACTTTGTATCCGACAGTGACCGGGCCAA 1424

QY 1651 TTATATGATGCAAAACACACAGTGCAGTGGCAGTTCCGAGAGAAAGCCAAAGCTCTGCATG 1710
    |||||
DB 1425 GCCTACGATGAGATGAGCAATGCCGTTTCAAGCATGAGTCAAAATCGCTAGTGTAAA 1484

QY 1711 CTGGACTTTAAAAAGACATCTGTAAAGCCCTGTGTGTCATCGTATTGGAAGGAATGT 1770
    |||||
DB 1485 TACG-----GGAGGTCTGCAAGGAGTGTGTCTGAGCAAGAAGCAACCGGTGC 1535

QY 1771 GAGACTAAATTTATGCCAGCAGAGAAGGACAAATTTGTGG-----CATGACATG 1821
    |||||
DB 1536 ATCAACCAACAGCATCCCGCGCGGAGGCAAGCTGTGCAAGCAGACACCATCGACAAG 1595

QY 1822 TGGTGCCGGGAGGACAGTGTGTGAATATGTGATGAAGCCCAAGCCCAAGCCCATGGC 1881
    |||||
DB 1596 GGGTGTGTCTACAACAGGCTGTGTCTCCCTTTGGGTGCGGCCCAAGAGGTGTGACGGA 1655

QY 1882 CACTGTGCGACTGCTTCTTTGTGTCCTCCATGCTCCAGAGCTGCGAGGGGAGTATCT 1941
    |||||
DB 1656 GCCTGGGGGCGGTGGAATCCATGGGGGCGACTGCAAGCCGACCTGTGCGGGCGCTGTCC 1715

QY 1942 CATAGAGTCCGCTCTGCACCAACCCCAAGCCATCGCATGAGGGGAAGTTCTGTGAGGC 2001
    |||||
DB 1716 TCTTCTAGCGGTCACTGCGAGAGCCCGGCAACCATCGGGGCAAGTACTGTCTGGGT 1775
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QY 2002 TCCACTCGCACTCTGAAGCTCTGCAACAGTCAAGAAATGTCCCCGGGACAGTGTGACTTC 2061
    |||||
DB 1776 GAGAGAAGCGGGACACCGCTCTCTGCAACACGAGATGACTGTCTCCCGTGGCTCCAGACTTC 1835

QY 2062 CGTGTGCTCAAGTGTGCCGAGCACAACAGCAGACGATTCAGAGGGCGGCACTACAAAGTGG 2121
    |||||
DB 1836 AGAGAAGTGCAGTGTCTTCAATTTGACAGCATCCCTTTCCGTGGGAAATTTCACAAGTGG 1895

QY 2122 AAGCTTACACTCAAGTAGAAGATCAGACTTATGCAAACTTACTGTATCGCAGAAAGGA 2181
    |||||
DB 1896 AAAACGTACCGGGGAGGGGCGGTGAAGGCC--TGCTCGCTCACGTGCTTACGCGAAAGGC 1952

QY 2182 TTTGATTTCTTCTTTTCTTTGTCMAATTAAGTCAAAAGATGGACTCCATGCTCGAGAGAT 2241
    |||||
DB 1953 TTCAACTTCTACACGAGAGGGCGGCGAGCCGTGTGTGACGCGGACACCTTGCCGTCCAGAC 2012

QY 2242 AGCCGTATGTTGTATATAGATGGATATGTGAGAGAGTTGATGTGACAAATGTCCTTGA 2301
    |||||
DB 2013 ACGGTGACATTTTGCCTGAGTGGCGAATGCAAGCACGTGGGCTGCGACCGAGTCTTGCGC 2072

QY 2302 TCTGATGCTGTGAAGACGCTCTGTGGGTGTGTAAAGGGAATTAAGTCAAGCTTCACGAT 2361
    |||||
DB 2073 TCCGACCTCGGGAGGAGCAAGTGCAGAGTGTGTGGCGGTGACGGCAGTGTCTGCGAAGCC 2132

QY 2362 CACAGGGGTCTCTACACCAAGCACCAACCAACCAAGTATTAACATGATGTCACCAT 2421
    |||||
DB 2133 ATCAGAGGGGTCTTACAGCCCAAGCTCACCTGAGGGCGGGTACGAGATGTCTGTGAT 2192

QY 2422 CTTCTGAGCCCGGAGATATCCGATCTATGAATGAAGTCTCTACCTTCTACATTTCT 2481
    |||||
DB 2193 CCCAAAGGCTCCGTCCACATCTTCATCCAGATCTGAACCTCTCTCTGATCACTTGGCC 2252

QY 2482 GTGGCAATGCCCTCAGAAAGTACTACTGTAATGGGCACTGGACCGTGAAGTGGCCGGC 2541
    |||||
DB 2253 CTGAAGGAGACCAAGAGTCCCTGCTGTGAGAGGGCTGGCCCGGAGACCCCGGAGCCCGC 2312

QY 2542 CGGTACAAATTTTGGGCACTACTTTGCACTACAGACGCTCTATATGAGCCCGAGAAC 2601
    |||||
DB 2313 CGTCTGCTCTAGCTGGGACCACTTTCACTGCGACAGGGGGCCAGACCAAGTCCAGAGC 2372

QY 2602 TTAATCGCTACTGAGCAACCAACGAGACACTGATTTGGAAGTGTG 2649
    |||||
DB 2373 CTGAAGCCCTGGAGCGATTAATGATCTCTCATGTGATGTGTG 2420
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RESULT 11
US-09-392-184-5/c
; Sequence 5, Application US/09392184
; Patent No. 6395889
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; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN
; FILE REFERENCE: 5800-55
; CURRENT APPLICATION NUMBER: US/09/392,184
; CURRENT FILING DATE: 1999-09-09
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; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 5357
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(5357)
; OTHER INFORMATION: repolysin (ADAM family of metalloprotease)
; NAME/KEY: misc_feature
; LOCATION: (1)...(5357)
; OTHER INFORMATION: n = A,T,C or G
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US-09-392-184-5
Query Match      7.1%; Score 204.6; DB 3; Length 5357;
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Best Local Similarity 50.9%; Pred. No. 9.6e-49;
Matches 787; Conservative 0; Mismatches 714; Indels 44; Gaps 11;

QY 1258 CATGACACGCGCATCTTACTGACTGCTGTGATATATGTTCTTGAGAAATGAGCCCTGT 1317
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 4316 CATGACACTGCCATCTCTGCTCACCAAGAAAGACCTGTGTGACAGCCATGAACCGGCTGT 4257
QY 1318 GACACTTGGGATTGGCAACCCATAGTGAATGTGTAGTAAATATCGCAGCTGCAGATT 1377
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 4256 GAGACCTGGGACTGTCCATGTGCGGGCATGTGCCAGCCGACCGCAGCTGCAGCATC 4197
QY 1378 AATGAAGATACAGGTCTTGAGCTGGCCTTCAACCATTTGCCATGAGCTTGACACAATT 1437
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 4196 AACGAGACACGGGCTGCCGCTGGCCTTCACTGTAGCCCAAGCAGCTCGGACAGTTT 4137
QY 1438 GGCATGATTCATATGAGAAAGGCAATGTGTAAAGTCCGAG-----GGCAACATC 1491
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 4136 GGCATTGACATGACGGAAGCGGCAATGACTGTAGCCCGTTGGGAAACGACCTTTTCATC 4077
QY 1492 ATGTCCCTACATTTGGCAGGACCGCATGAGTCTTCTCTGTGTCACCTGCAGCGCCAG 1551
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 4076 ATGTCTCCACAGCTCTGTACGACGCGCTCCCTCCATCCTGTGTCGCTGCAGCGCCAG 4017
QY 1552 TATCTACACAATTTCTAAGCAGCGCTCAAGCTATCTGCTTGTGATCAGCCAAAGCCT 1611
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 4016 TATATCACCAAGTTCCTTGACCGTGGGTGGGCTGTGCTGCGACGACCTTC---TGCC 3960
QY 1612 GTGAAGAAATACAGATATCTTGAGAAATTTGCCAGAGAAATTATATGATGCAACACAG 1671
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 3959 AAGACATTATGACTTCCCTCGGTGCCACCTGGCGTCTCTATGATGTAAGCCACAG 3900
QY 1672 TGCAGGTGCGAGTTCGAGAGAAAGCCAGCTGTCATGCTGCACTTAAAAAGACATC 1731
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 3899 TGCGGCTCCAGTACGGGGCTTACTGTGCTTCTGC-----GAGACATGATAATGTC 3846
QY 1732 TGTAAAGCCCTGTGTGCTCATCTGTAATGGAAGAAATGTAGACTTAATTATGCCAGCA 1791
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 3845 TGCCACACACTGTGTGC--TGTGTGGGAGCACACTGTCACTCCAGCTGATGCAAGCCC 3788
QY 1792 GCGAAGGCACAATTTGTGGGATGACATGTGTGCCGGGAGGACAGTGTGTAATAT 1851
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 3787 GTGACGCGCACCGGTGTGGGAGAAATAAGTGTGTCTCAGTGGGAGTGCCT---ACCC 3731
QY 1852 GGTGATGAAGGCCCCAAGCCACCCATGGCAGTGTGCTGCTTCTTGTGCCCCA 1911
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 3730 GTGGGCTTCCGGCCGAGGCGGTGATGTGTGCTGTGCTGAGCGCCTGTGCATC 3671
QY 1912 TGTCCAGGACCTGCGGAGGGGAGTATCTCATAGAGTGCCTCTGCACCAACCCCAAG 1971
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 3670 TGTCTACGAGCTGTGGCATGGGGTACAGAGCGCGGAGTGCAGCGCCTAGC 3611
QY 1972 CCATCGCATGAGGGAAGTCTGTGAGGGCTCAGCTCGCACTTGAAGCTTGAACAGT 2031
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 3610 CCCAATACAAAGGCAAGATACGTGTGTGGTGAAGCGCAAGCGCTTCCGCTTGAACCTG 3551
QY 2032 CAGAAATGTCCCGGGAAGTGTGACTTCCGTGCTGCTCAGTGTGCCGAGCAACAGC 2091
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 3550 CAGGCTGCGCTGTGGCGCGCCCTCTTCCGCACTCAGTGCAGCCACTTGAAGCT 3491
QY 2092 AGACGATTCAAGGGCGGCACTACAGTGAAGCTTACACTCAAGTAGAAGATCAGAC 2151
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 3490 ATGCTCTACAAGGCGCAGCTGCACATGGGTG-----CCGTGTCAATGACGTGAC 3437
QY 2152 TTATGCAAACTTACTGTATCGCAGAAGATTGATTTCTTTCTTTGTGAATAA 2211
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 3436 CCTGCGAGCTGCACTGCCGCGCGCAATGAGTACTTTGCCGAGAAGCTGCCGAGCC 3377
QY 2212 GTCAAGATGGGACTCCATGCTCGAGGAT-----AGCCGTAATGTTTGTATGATGG 2265
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 3376 GTGTGATGGCAACCCCTGCTACAGGTCCGAGCAGCCGGGACCTCTGCATCAAGGC 3317
QY 2266 ATATGTGAGAGTTGATGTGACAAATGCTTGTGATCTGATGCTGTGAAGACTCTGT 2325
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DB 3316 ATCTGTAAAGACGTGGCTGTGACTTCAAGATTGACTCCGCTGTATGAGAGACCGCTGT 3257
QY 2326 GGGGTGTGTAACGGAAATACCTCAGCCTGCAGATTCAAGGGGTCTCTACCAAGCAC 2385
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 3256 GGTGTGCGCACGGCAACGGCTCCACCTGCACACCGTGAGCGGAGACTTGC---AGAG 3200
QY 2386 CACCACACCAACAGTATTAATCATGTGTACACCATTCCTTCTGAGGCCCGAGTATCCGC 2445
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 3199 GCCAGAGGCGCTGGGTATGTGATGTGGGTGATCCAGCGCGGCGCAGCAGATCCGC 3140
QY 2446 ATCTATGAATGAAAGCTCTTCACTCCTCACTTAATTCCTGTGCGCA--ATGCCCTAGAAG 2502
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 3139 ATCCAAGAGTTGCCAGAGCTGCCAATCTCTGGCACTGCGAGTGAGACCCGAGAAG 3080
QY 2503 TACTACCTGAATGGGCACTGACCGGTGACTGGCCCGCGGTACAATTTTGGGCACT 2562
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 3079 TACTTCTCATGTGTGCTGACCATCCAGTGAACGGGACTACAGGTGGCAGGACC 3020
QY 2563 ACTTTCGACTACAGACGGTCTTATATGAGCCCGAGAACTTAATCGCTACTGACCAACC 2622
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 3019 ACCTTCACTACGACACGACGGGCAACTG---GAGAACTCAAGTCCCGGCTCCACC 2963
QY 2623 AACGAGACATGATGTGAGCTGTCTGTTCAAGGAGAAACCCGGGTGTGCTGGAA 2682
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2962 AAGGAGCTGTGTGATCCAGTGTCTGTTCAGAGAGACAACTGGGTGCACTACAG 2903
QY 2683 TACTCCATGCTCGCTTGGGACCGAGACAGCCCCCTGCCAGCCCACTACACTTG 2742
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2902 TACACCATCCACAGGAGGAGGTGCCACGACGAGTCCCGCCGCGCTGTCTCTGG 2843
QY 2743 GCCATGCTGCGCT---CTGAGTGTCTCCGTGCTGCGGAGGGGT 2784
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2842 CATATGAGGCTTGACCAAGTGCACAGTCACTCGCGCAGAGT 2798

RESULT 12
US-09-981-953A-1
; Sequence 1, Application US/09981953A
; Patent No. 6689599
; GENERAL INFORMATION:
; APPLICANT: RACIE, LISA A.
; APPLICANT: TWINE, NATALIE C.
; APPLICANT: AGOSTINO, MICHAEL J.
; APPLICANT: WOLFMAN, NEIL
; APPLICANT: MORRIS, ELISABETH A.
; TITLE OF INVENTION: NOVEL AGGREGANASE MOLECULES
; FILE REFERENCE: 08702.0075-00000
; CURRENT APPLICATION NUMBER: US/09/981, 953A
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/242,317
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3766
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Nucleotide
US-09-981-953A-1

Query Match 7.0%; Score 201.6; DB 4; Length 3766;
Best Local Similarity 49.1%; Pred. No. 5.8e-48;
Matches 701; Conservative 0; Mismatches 694; Indels 33; Gaps 5;

QY 1240 GGGAAAGATGGGACTGTGATGACCAAGCCATCTTACTGACTGTGTGATATATGTTCC 1299
DB 1251 GAGAACGTTGTGCTAACCAATGACACAGCAGTGTCTATACACGCTATGACATCTGCATC 1310
QY 1300 TGAAGAATGAGCCCTGTGACACTTTGGGATTTGCACCCATAAGTGAATGTGTGTA 1359
DB 1311 TACAAGAACAAACCTTGGCGCACACTAGGCTGTGCGCGGTGGCGGAATGTGTAGCGC 1370
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QY 1360 TATCGACGTGCAAGTAAATGAGATACAGTCTTGAGACTGGCTTACCATTGGCCAT 1419
Db 1371 GAGAGAAGCTGACGCGTCAATGAGACATTGGCTGGCCACAGCGTTCAACCAATTGCCAC 1430
QY 1420 GAGTCTGACACAACTTTGGCATGATTTCATGATGAGAAGGAAACATGT-----GT 1470
Db 1431 GAGATCGGGACACATTCGGCATGAGACCATGACGCGTGGGAAACAGCTGTGGGGCCCGT 1490
QY 1471 AAAAAGTCCGAGGCAACATCATGTCCCTACATTGGCAGAGCGCAATGAGTCTTCTCC 1530
Db 1491 GGTCAAGAGCCAGCCAGCTCATGGCTGCCACATTACCATGAGAACCACCATTCGTG 1550
QY 1531 TGGTCACCTCGACCGCCAGTATCTACACAAATTTCTAAGACCCGCTCAGCTATCTGC 1590
Db 1551 TGGTCATCCTGACCGCGTGACATCACCAAGCTTTCTAGACTCAGGGCCCTGGGGCTCTG 1610
QY 1591 CTTGCTGATCAGCCAAAGCCTGTGAAGGAATACAGTATCCTGAGAAATTGCCAGAGAA 1650
Db 1611 CCTGAACAACCGGCC--CCCAAGACAGGACTTGTGTACCCGACAGTGGCACCGGCCAA 1668
QY 1651 TTATATGATGCAAAACACAGTGCAGTGGCAGTTCGGAAGAAAGCCAGCTTCGATG 1710
Db 1669 GCCTACGATGCAGATGAGCAATGCCGCTTTCAGCATGAGTCAAAATCGCGTACGTGA-- 1726
QY 1711 CTGGACTTTAAAGGACATCTGTAAAGCCCTGTGTGTCCTCATCTATTGGAAGAAATGT 1770
Db 1727 -----AATACGGGAGGTCTGTCAAGCGAGCTGTGTCTGTAGCAAGAGCAACCGGTGC 1778
QY 1771 GAGACTAAATTTATGCCAGCAGAGAAAGGCAAAATTTGTGGCA-----TGACATG 1821
Db 1779 ATCAACCAACAGATCCCGGCCGCGGAGGCGACGCTGTGCCAGACGACACCATCGACAAG 1838
QY 1822 TGGTCCCGGGAGGACAGTGTGTGAATATGTGTGATGAAGGCCCAAGCCCAACCATGGC 1881
Db 1839 GGGTGGTGTCTACAAACGGGTCTGTGTCCCTTTGGGTGCGGCCCAAGAGGTTGGAACGA 1898
QY 1882 CACTGGTCCGACTGCTCTTCTTGGTCCCATGCTCCAGAGCCTGCGGAGGGGAGTATCT 1941
Db 1899 GCCTGGGGGCGGTGGACTCCATGGGGGCGACTGTGCAGCCGGAACCTGTGGCGGCGGTGCC 1958
QY 1942 CATAGAGTCCGCTCTGCACCAACCCCAAGCCATTCGCATGAGGGAAGTTCTGTAGGGC 2001
Db 1959 TCTTCTAGCCGTCACTGCGACAGCCCCAGGCCAACCATCGGGGCAAGTACTGTGGGT 2018
QY 2002 TCCACTCGCACTCTGAAGCTCTGCAACAGTCAAGTAATGTCCCCGGGACAGTGTGACTTC 2061
Db 2019 GAGAGAAGGCGGCAACCGCTCTGCAACACGAGTGACTGTCCCCCTGGCTCCAGGACTTC 2078
QY 2062 CGTGTGCTCAAGTGTGCCGAGCAACACAGCAGATTCAGAGGGCGGCACTACAAGTGG 2121
Db 2079 AGAGAAGTCAAGTGTTCGAATTTGACAGCATCCCTTCCGTGGGAAATTTTACAAGTGG 2138
QY 2122 AAGCCTTACACTCAAGTAGAAGATCAGGACTTATGCAAACTCTACTGTATGCAAGAGA 2181
Db 2139 AAAACGTACCGGGGAGGGGGCGTGAAGGCC--TGCTCGCTCACTGCTAGCGGAAGGC 2195
QY 2182 TTTGATTTCTTCTTTTCTTTGTCAATAAAGTCAAAAGATGGAATCCATGCTCGGAGAT 2241
Db 2196 TTCAACTTCTACACGAGAGGGCGGAGCCGTGTGTGACGGGACACCCCTGCGTCCAGAC 2255
QY 2242 AGCCGTAATGTTTGTATAGATGGGATATGTGAGAGAGTGTGATGTGACAAATGCTTGA 2301
Db 2256 ACGGTGACATTTGCGTCAGTGGCGAATGCAAGCACGTGGGCTGCGACCGAGTCTTGGGC 2315
QY 2302 TCTGATGCTGTTGAAGACGTCTGTGGGTGTGTAAACGGGAATTAATCAGCTGCAGAT 2361
Db 2316 TCCGACCTGCGGAGAGACAAGTGCAGAGTGTGTGGCGGTGACGGCAGTGCCTGCGAGACC 2375
QY 2362 CACAGGGGTCTTACACCAAGCACACCAACCAACAGTATTAATCATAGTGCACCAT 2421
Db 2376 ATCAGGGGCGTCTTACGCCACGCTCACCTGGGGCGGGTACGAGATGTCTGTGATT 2435
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QY 2422 CTTCTGAGCCCGGAGTATCCGCATCTATGAATGAACGTCTCTACTCTTACATTTCT 2481
Db 2436 CCCAAGGCTCCGTCCACATCTTCAATCCAGATCTGAACCTCTCTCACTGCACTTGCC 2495
QY 2482 GTGCGAAATGCCCTCAGAAAGTACTACTGAATGAGGCACTGGACCGTGAACGCGCCG 2541
Db 2496 CTGAAGGAGACAGAGATCCCTGCTGTGTGAGGGGTGCCCGGAGCCCGGACCCAC 2555
QY 2542 CGGTACAAATTTTCGGCACTACTTTGCACTACAGACGCTCCTAATGAGCCGAGAAC 2601
Db 2556 GGTGCTCTTAGCTGAGACCACTTTCACTGCGACAGGGGCCAGACAGTCCAGAGC 2615
QY 2602 TTAATCGTACTGAGCAACCAACGAGACACTGATTTGAGCTGCTG 2649
Db 2616 CTCGAAGCCCTGGACCGATTAATGCAATCTCTCATGTCATGTGCTG 2663
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RESULT 13

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US-09-369-364A-6
; Sequence 6, Application US/09369364A
; Patent No. 6391610
; GENERAL INFORMATION:
; APPLICANT: Apte, Suneel
; APPLICANT: Hurskainen, Tiina L.
; APPLICANT: Hirohata, Satoshi
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; FILE REFERENCE: 26473/4007/10-30-00
; CURRENT APPLICATION NUMBER: US/09/369,364A
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 3218
; TYPE: DNA
; ORGANISM: Homo sapiens ADAMTS-7
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)..(3003)
US-09-369-364A-6
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Query Match 6.3%; Score 182.6; DB 3; Length 3218;
Best Local Similarity 50.8%; Pred. No. 1.9e-42;
Matches 714; Conservative 0; Mismatches 649; Indels 42; Gaps 10;

QY 1258 CATGACCAAGCCATCTTACTGACTGTCTGATATATGTTCTCTGAAGATGAGCCCTGT 1317
Db 1015 CATGACACTGCCATCTGCTCACCAGAAAGACCTGTGTGACAGCATGAACCGGCTGT 1074
QY 1318 GACACTTTGGGATTTGCAACCCATAAGTGAATGTGTAGTAATATCGAGCTGCAGATT 1377
Db 1075 GAGACCTGGGACTGTCCCATGTGTGGGGCATGTGCCAGCCGACCGGAGCTGCAGATC 1134
QY 1378 AATGAAGTACAGGTCTTGGACTGGCCTTCAACCATTCGCATGAGTCTGACACAACATTT 1437
Db 1135 AAGGAGACAGGGCTCGCTGAGCGCTTCACTGTAGCCACGAGCTGGGACAGATTTT 1194
QY 1438 GGCATGATTCATGATGAGAGAGGAAATGTGTAAAGTCCGAG-----GGCAACATC 1491
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QY 1492 ATGTCCCTACATTTGCGAGACGCAATGAGTCTTCTCCTGTGTCAACCTGCAGCCGCGAG 1551
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QY 1552 TATCTACACAATTTCTAAGCACCGCTCAAGCTATCTGCCTTGTGCTGATCAGCCAAAGCT 1611
Db 1315 TATATCACCAAGTTCCTTGAACCGTGGGTGGGCTGTGCTGGAACGACCTCTCT--GCC 1371
QY 1612 GTGAAGGAATACAAAGTATCTGAGAAATTCGCAAGAGAAATTAATATGCAAAACACAG 1671
Db 1372 AAGGACATTAATGACTTCCCTCGGTGCCACCTGGCGTCTCTATATGTAAGCCACCAAG 1431
QY 1672 TGCAAGTGGCAATTGGAAGAGAAAGCAAGCTCTGCAATGCTGACTTTAAAAAGACATC 1731
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Db 1432 TGCCGCCCTCCAGTACGGGGCCCTACTCTGCCCTTCTGC-----GAGGACATGATAATATGTC 1485
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Qy 1912 TGCTCCAGGACCTGCGGAGGGGAGTATCTCATAGGAGTGCCTCTGCACCAACCCCAAG 1971
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Qy 2212 GTCAAGATGGGACTCCATGCTCGAG-----GATAGCCGTAACTTTGTAATAGTGG 2265
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Qy 2266 ATATGTAGAGAGTTGGATGTGACATGTCTTGGATCTGTGATGCTGTGAAGAGCTGTGT 2325
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Db 2368 AAGGAGCCTGTCTGATCCAGGTGC 2392

RESULT 14
US-09-369-364A-16
; Sequence 16, Application us/09369364A
; Patent No. 6391610
; GENERAL INFORMATION:

; APPLICANT: Apte, Suneel
; APPLICANT: Hurskainen, Tiina L.
; APPLICANT: Hirohata, Satoshi
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; FILE REFERENCE: 26473/4007/10-30-00
; CURRENT APPLICATION NUMBER: US/09/369,364A
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 3885
; TYPE: DNA
; ORGANISM: Homo sapiens ADAMTS-10
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3246)
; NAME/KEY: misc feature
; LOCATION: (3877)
; OTHER INFORMATION: n=A
; NAME/KEY: misc feature
; LOCATION: (3882)
; OTHER INFORMATION: n=C
US-09-369-364A-16

Query Match 6.1%; Score 176.8; DB 3; Length 3885;
Best Local Similarity 49.4%; Pred. No. 1.1e-40;
Matches 705; Conservative 0; Mismatches 687; Indels 36; Gaps 8;

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RESULT 15
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; Sequence 4, Application US/09369364A
; Patent No. 6391610
; GENERAL INFORMATION:
; APPLICANT: Apte, Suneel
; APPLICANT: Hurskainen, Tiina L.
; APPLICANT: Hirohata, Satoshi
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; FILE REFERENCE: 26473/4007/10-30-00
; CURRENT APPLICATION NUMBER: US/09/369,364A
; CURRENT FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2848
; TYPE: DNA
; ORGANISM: Homo sapiens ADAMTS-6
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (22)..(2601)
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; NAME/KEY: misc feature
; LOCATION: (1369)
; OTHER INFORMATION: n = C
; NAME/KEY: misc feature
; LOCATION: (1620)
; OTHER INFORMATION: n=C
US-09-369-364A-4
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Query Match 5.0%; Score 144; DB 3; Length 2848;
Best Local Similarity 48.5%; Pred. No. 3.6e-31;
Matches 464; Conservative 0; Mismatches 481; Indels 12; Gaps 2;
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Db 1510 GGAGATTGTGTTCTTTTGGCACTTGGCCCCAGAGCATAGATGGGGCTGGGCTCCCTGG 1569
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Db 1630 TGTGACAGTCCAGCACTTCGAGGTGAAAAAATATGCTTGGGAAAAAGAAACGGTAT 1689
QY 2017 AAGCTCTGCAACAGTCAAGAAATGTCCCGGGACAGTGTGACTTCCGTGCTCAGTGT 2076
Db 1690 CGCTCTGTAAACACAGATCCATGCTTGTGGGTTCCGAGATTTTCAGAGAAACAGTGT 1749
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Db 1807 GGAGTGGGTAAACCTTGTGATTAACCTGCTGGAAGTTAATTTCTACTACT 1866
QY 2197 TCTTGTCAATTAAGTCAAAAGATGGGACTCCATGCTCGAGAGATAGCGTAATGTTGT 2256
Db 1867 GAACGTCTCTCGCGGTGATCGATGGGACCAAGTCAATGCGATTCACTGATATCTGC 1926
QY 2257 ATAGATGGATATGTGAGAGAGTGTGATGACAATGCTTGTGATGTGATGCTTGA 2316
Db 1927 ATCAATGGAATGCAAGCAGTAAAGCTGTGATTAATTTTGGATCTGATGCTAGGAA 1986
QY 2317 GACGTGTGGGGTGTGTAACGGAATTAACAGCTGCAAGATTACAGGGGCTCTAC 2376
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QY 2557 GGCACTACTTTGCACTACAGACGGTCTATAATGAGCCGAGAACTTAATCGCTACTGGA 2616
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Db 2287 CCTACCTCAGAAATCTCATCGTCATGGTTCTCTCTCAAGACAGAAATTTGGGAATT 2343

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Job time : 510 secs



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OM protein - protein search, using sw model

Run on: September 9, 2005, 11:45:44 ; Search time 267 Seconds
(without alignments)
266.164 Million cell updates/sec

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Perfect score: 5236
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Scoring table: BLOSUM62
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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3846.5	73.5	1224	4	US-09-930-872-4	Sequence 4, Appl1
2	3846.5	73.5	1224	4	US-10-217-774-4	Sequence 4, Appl1
3	1543.5	29.5	491	4	US-09-930-872-2	Sequence 2, Appl1
4	1543.5	29.5	491	4	US-10-217-774-2	Sequence 2, Appl1
5	1390	26.5	908	4	US-09-963-791-2	Sequence 2, Appl1
6	1319	25.2	757	4	US-09-963-791-24	Sequence 24, Appl1
7	1243	23.7	1104	4	US-09-981-953A-4	Sequence 4, Appl1
8	1188	22.7	859	3	US-09-369-364A-5	Sequence 5, Appl1
9	1179	22.5	997	3	US-09-369-364A-7	Sequence 7, Appl1
10	1057.5	20.2	1081	3	US-09-369-364A-17	Sequence 17, Appl1
11	1056	20.2	1882	3	US-09-369-364A-13	Sequence 13, Appl1
12	1022.5	19.5	950	4	US-09-321-987B-4	Sequence 4, Appl1
13	1022	19.5	770	4	US-09-981-953A-2	Sequence 2, Appl1
14	991	18.9	874	3	US-09-369-364A-15	Sequence 15, Appl1
15	984.5	18.8	967	4	US-09-130-491-2	Sequence 2, Appl1
16	982.5	18.8	949	4	US-09-568-559-2	Sequence 2, Appl1
17	969	18.5	2150	4	US-09-321-987B-2	Sequence 2, Appl1
18	965.5	18.4	2165	4	US-09-800-729-155	Sequence 155, App
19	958.5	18.3	727	4	US-09-445-023A-12	Sequence 12, Appl1
20	949	18.1	1211	4	US-09-949-016-11401	Sequence 11401, A
21	948	18.1	969	4	US-09-321-987B-5	Sequence 5, Appl1
22	934	17.8	727	4	US-09-445-023A-1	Sequence 1, Appl1
23	933	17.8	1205	4	US-09-491-522-11	Sequence 11, Appl1
24	929.5	17.8	950	4	US-10-009-332-1	Sequence 1, Appl1
25	923	17.6	1211	4	US-09-491-522-5	Sequence 5, Appl1
26	903	17.2	608	4	US-09-130-491-13	Sequence 13, Appl1
27	885.5	16.9	930	3	US-09-369-364A-2	Sequence 2, Appl1

28	878	16.8	930	4	US-09-122-126B-15	Sequence 15, Appl1
29	878	16.8	930	4	US-09-634-286A-15	Sequence 15, Appl1
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34	823.5	15.7	905	3	US-09-369-364A-9	Sequence 9, Appl1
35	778.5	14.9	551	4	US-09-130-491-16	Sequence 16, Appl1
36	776.5	14.8	589	4	US-09-963-791-12	Sequence 12, Appl1
37	705.5	13.5	438	4	US-09-963-791-22	Sequence 22, Appl1
38	675.5	12.9	518	3	US-09-369-364A-22	Sequence 22, Appl1
39	607	11.6	481	4	US-09-130-491-8	Sequence 8, Appl1
40	578.5	11.0	507	4	US-09-963-791-10	Sequence 10, Appl1
41	550	10.5	1039	4	US-09-949-016-7859	Sequence 7859, Ap
42	507.5	9.7	356	4	US-09-963-791-20	Sequence 20, Appl1
43	476.5	9.1	446	4	US-09-784-358-4	Sequence 4, Appl1
44	476.5	9.1	724	4	US-09-784-358-8	Sequence 8, Appl1
45	476.5	9.1	845	4	US-09-784-358-12	Sequence 12, Appl1

ALIGNMENTS

RESULT 1									
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; Sequence 4, Application US/09930872									
; Patent No. 6448388									
; GENERAL INFORMATION:									
; APPLICANT: Fiddie, Carl Johan									
; APPLICANT: Hilbun, Brian									
; TITLE OF INVENTION: No. 6448388e1 Human Proteases and Polynucleotides Encoding the San									
; FILE REFERENCE: LEX-0219-USA									
; CURRENT APPLICATION NUMBER: US/09/930,872									
; CURRENT FILING DATE: 2001-08-14									
; PRIOR APPLICATION NUMBER: US 60/225,852									
; PRIOR FILING DATE: 2000-08-16									
; NUMBER OF SEQ ID NOS: 5									
; SOFTWARE: FastSeq for Windows Version 4.0									
; SEQ ID NO 4									
; LENGTH: 1224									
; TYPE: PRT									
; ORGANISM: homo sapiens									
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Best Local Similarity 75.4%; Pred. No. 0;									
Matches 738; Conservative 25; Mismatches 73; Indels 143; Gaps 13;									
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DB	172	R-----TEBADYFLRPLPSHLSWL-GRAAQSSPSHVLTKRSTEPHAGASEVLVT	222						
QY	292	AEGFDFPFFS--LSNKVKDGTGCESDSRNVCIDGICELSVSTSAHMPQRPKEDLFLPDE	349						
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QY 668 TLKLCNSQKCPRDSVDFRAQCAEHNSRRFRGRHYKMKPYQVEDQDLCKLYCIAEGFDF 727
Db 631 TLKLCNSQKCPRDSVDFRAQCAEHNSRRFRGRHYKMKPYQVEDQDLCKLYCIAEGFDF 690
QY 728 FFSLSNKKVDCGTPCSEDSRNVCIDGICERVGCDNVLGSDAVEDVCGVCNGNNSACTIHRG 787
Db 691 FFSLSNKKVDCGTPCSEDSRNVCIDGICERVGCDNVLGSDAVEDVCGVCNGNNSACTIHRG 750
QY 788 LYTKEHHTNQYHMTIIPSGARSIRIYEMNVSTYSVRNALRRYYLNGHWTVDWPGRYK 847
Db 751 LYTKEHHTNQYHMTIIPSGARSIRIYEMNVSTYSVRNALRRYYLNGHWTVDWPGRYK 810
QY 848 FSGTTFDYRRSYNEPENLIATGPTNETLIVELLFQGRNPGVAMEYSMPRLGTEKQPPAOP 907
Db 811 FSGTTFDYRRSYNEPENLIATGPTNETLIVELLFQGRNPGVAMEYSMPRLGTEKQPPAOP 870
QY 908 SYTWAIVRSECSVSCGGGR 926
Db 871 SYTWAIVRSECSVSCGGGQ 889
```

```
RESULT 2
US-10-217-774-4
; Sequence 4, Application US/10217774
; Patent No. 6734007
; GENERAL INFORMATION:
; APPLICANT: Fridde, Carl Johan
; APPLICANT: Hilbun, Erin
; TITLE OF INVENTION: No. 6734007el Human Proteases and Polynucleotides Encoding the
; FILE OF INVENTION: Same
; FILE REFERENCE: LEX-0219-USA
; CURRENT APPLICATION NUMBER: US/10/217,774
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US/09/930,872
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,852
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1224
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-217-774-4
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Query Match 73.5%; Score 3846.5; DB 4; Length 1224;
Best Local Similarity 75.4%; Pred. No. 0;
Matches 738; Conservative 25; Mismatches 73; Indels 143; Gaps 13;
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QY 1 MKPRARGWGLAALMMLLAQVAEQVSPGRSHQRGNRSGQLEASPRLLSRGPRRLTAMS 60

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Db 1 MKPRARGWGLAALMMLLAQVAEQAP-----ACAMG 31
QY 61 PLFSAGTCVRHGTSSGSAWPPERPASSSTRGAAGLDGKGRDMDGAGNHSQQTNTGTENQ 120
Db 32 PAAAA-----PGSPSVPRPPPPAERPG-----WMEKG----- 58
QY 121 TLHLVTOYDLVSAYEVDRGDYVSHEIMHQRRRAVAVSEVESLHLRLKGRHDFHMDL 180
Db 59 -----EYDLVSAYEVDRGDYVSHEIMHQRRRAVAVSEVESLHLRLKGRHDFHMDL 112
QY 181 RTSSSLVABGFIYQTLGKTGTSVQTLPPEDFCFYQGSLSRHSNPSHGKFCBGSTRTL 240
Db 113 RTSSSLVABGFIYQTLGKTGTSVQTLPPEDFCFYQGSLSRHSNPSHGKFCBGSTRTL 171
QY 241 KLCNSQKCPRDSVDFRAQCAEHNSRRFRGR-----HYKMKPYQVEA-DLCKLYCI 291
Db 172 R-----TEADYFLRPLPSHLSWKL-GRAAQSSPSHVL YKRSTEPHAPGASEVLVT 222
QY 292 AEGFDFFS--LSNKVDCGTPCSEDSRNVCIDGICELSVSTSAHMPQPEKEDLFIIPDE 349
Db 223 SRTWELAHQPLHSSDLRLGLP--QKHFC-----GRKKYMPQPEKEDLFIIPDE 270
QY 350 YKSLRHKRSLRSHRNEELNVELLVVDKQWQNHGHENITTYVLTILNMVSALFKD-- 407
Db 271 YKSLRHKRSLRSHRNEELNVELLVVDKQWQNHGHENITTYVLTILNMVSALFKDGT 330
QY 408 -----GLMKDGTGRDHAILLTGLD 427
Db 331 ICGNINIAIVGLLLEDEQPLVISHADHTLSSFCQWQSGLMGKDGTGRDHAILLTGLD 390
QY 428 ICSWKNEPCDTLGFAPISGMSKRYRSCCTINEDTGLAFTIAHESGHNFGMIHDEGNMC 487
Db 391 ICSWKNEPCDTLGFAPISGMSKRYRSCCTINEDTGLAFTIAHESGHNFGMIHDEGNMC 450
QY 488 KKSEGNIMSPFLAGRNGVFSWSPCSRQYLHKFLSTAQAICLADQPKPYKEYKYPEKLPG 547
Db 451 KKSEGNIMSPFLAGRNGVFSWSPCSRQYLHKFLSTAQAICLADQPKPYKEYKYPEKLPG 510
QY 548 LYDANTQCKWQFGEKAKLCMLDFKKDICKALMCHIRIGRKCEETKFMPAEAGTICGHDMMCR 607
Db 511 LYDANTQCKWQFGEKAKLCMLDFKKDICKALMCHIRIGRKCEETKFMPAEAGTICGHDMMCR 570
QY 608 GGQCVKYGDEGPKPTHGHWSDMSSWSPCSRTCGGGVSHRSRLCTNPKPSHGKFCBGSTR 667
Db 571 GGQCVKYGDEGPKPTHGHWSDMSSWSPCSRTCGGGVSHRSRLCTNPKPSHGKFCBGSTR 630
QY 668 TLKLCNSQKCPRDSVDFRAQCAEHNSRRFRGRHYKMKPYQVEDQDLCKLYCIAEGFDF 727
Db 631 TLKLCNSQKCPRDSVDFRAQCAEHNSRRFRGRHYKMKPYQVEDQDLCKLYCIAEGFDF 690
QY 728 FFSLSNKKVDCGTPCSEDSRNVCIDGICERVGCDNVLGSDAVEDVCGVCNGNNSACTIHRG 787
Db 691 FFSLSNKKVDCGTPCSEDSRNVCIDGICERVGCDNVLGSDAVEDVCGVCNGNNSACTIHRG 750
QY 788 LYTKEHHTNQYHMTIIPSGARSIRIYEMNVSTYSVRNALRRYYLNGHWTVDWPGRYK 847
Db 751 LYTKEHHTNQYHMTIIPSGARSIRIYEMNVSTYSVRNALRRYYLNGHWTVDWPGRYK 810
QY 848 FSGTTFDYRRSYNEPENLIATGPTNETLIVELLFQGRNPGVAMEYSMPRLGTEKQPPAOP 907
Db 811 FSGTTFDYRRSYNEPENLIATGPTNETLIVELLFQGRNPGVAMEYSMPRLGTEKQPPAOP 870
QY 908 SYTWAIVRSECSVSCGGGR 926
Db 871 SYTWAIVRSECSVSCGGGQ 889
```

```
RESULT 3
US-09-930-872-2
; Sequence 2, Application US/09930872
; Patent No. 6448388
; GENERAL INFORMATION:
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APPLICANT: Friddle, Carl Johan
APPLICANT: Hilbun, Erin
TITLE OF INVENTION: No. 6448388e1 Human Proteases and Polynucleotides Encoding the Sa
FILE REFERENCE: LEX-0219-USA
CURRENT APPLICATION NUMBER: US/09/930,872
CURRENT FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: US 60/225,852
PRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 491
TYPE: PRT
ORGANISM: homo sapiens
US-09-930-872-2

Query Match 29.5%; Score 1543.5; DB 4; Length 491;
Best Local Similarity 57.7%; Pred. No. 2.2e-129;
Matches 333; Conservative 26; Mismatches 75; Indels 143; Gaps 13;

QY 1 MKPRARGWRLAALMMLAQAQVSPGRSHQGNRGSGGLEASPRLLSRGPRRLTAMS 60
Db 1 MKPRARGWRLAALMMLAQAQVSPGRSHQGNRGSGGLEASPRLLSRGPRRLTAMS 60
QY 61 PLFSAGTCVRHGTSSGSAWEPERPASSSTRGAAGLDGKGRDMEAGNHRSGQTNTGTENQ 120
Db 32 PAAAA-----PGSPSVPRPPPPAERPG-----WMEKG-----ACAMG 31
QY 121 TLHVLTYDYLVSAYEVDHREGDYVSHEIMHQRRRAVAVSEVSLHLRLKGRHDFHMDL 180
Db 59 -----EYDLVSAYEVDHREGDYVSHEIMHQRRRAVAVSEVSLHLRLKGRHDFHMDL 112
QY 181 RTSSSLVAPGFIQTGKTGTSVQTLPPEDFCFYOGSLRSHRNSPSHGKCEGSTRTL 240
Db 113 RTSSSLVAPGFIQTGKTGTSVQTLPPEDFCFYOGSLRSHRNS-SVALSTCGLSGMI 171
QY 241 KLCNSQKCPRDSVDFRAAQCAEHNSRRFRGR-----HYKMKPYTQVEA-DLCKLYCI 291
Db 172 R-----TEADYFLRPLPSHLISWKL-GRAAQSSPSHVLTKRSTEPHAPGASEVLVT 222
QY 292 AEGFDFFFS--LSNKVKDGTPCSEDSRNVCI DGCILSVSTSAHMPQPKEDLFI LPDE 349
Db 223 SRTWELAHQPLHSSDLRLGLP--QKHFC-----GRKKYMPQPKEDLFI LPDE 270
QY 350 YKSCLRHKRSLRSHRNEELNVETLVVVDKKMOMNHGHEINTTYVLTILNVSALFKD-- 407
Db 271 YKSCLRHKRSLRSHRNEELNVETLVVVDKKMOMNHGHEINTTYVLTILNVSALFKDGT 330
QY 408 -----GLMGKDGTGRHDAIILLTGLD 427
Db 331 IGGNINIAIVGLILLEDEQPLVISHHADHTLSSFCQWQSGLMGKDGTGRHDAIILLTGLD 390
QY 428 ICSWKNEPCDTLGFAPISGMSKYRSCCTINEDTGLGIAFTIAHESGHNFGMIHDGEGNMC 487
Db 391 ICSWKNEPCDTLGFAPISGMSKYRSCCTINEDTGLGIAFTIAHESGHNFGMIHDGEGNMC 450
QY 488 KKEGNI MSPTLA GRNGVFSWSPCSRQYLHKFLSTAQ 524
Db 451 KKEGNI MSPTLA GRNGVFSWSPCSRQYLHKFLRSVK 487

RESULT 4
US-10-217-774-2
Sequence 2, Application US/10217774
Patent No. 6734007
GENERAL INFORMATION:
APPLICANT: Friddle, Carl Johan
APPLICANT: Hilbun, Erin
TITLE OF INVENTION: No. 6734007e1 Human Proteases and Polynucleotides Encoding the
FILE REFERENCE: LEX-0219-USA
CURRENT APPLICATION NUMBER: US/10/217,774
CURRENT FILING DATE: 2002-08-12

PRIOR APPLICATION NUMBER: US/09/930,872
PRIOR FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: US 60/225,852
PRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 491
TYPE: PRT
ORGANISM: homo sapiens
US-10-217-774-2

Query Match 29.5%; Score 1543.5; DB 4; Length 491;
Best Local Similarity 57.7%; Pred. No. 2.2e-129;
Matches 333; Conservative 26; Mismatches 75; Indels 143; Gaps 13;

QY 1 MKPRARGWRLAALMMLAQAQVSPGRSHQGNRGSGGLEASPRLLSRGPRRLTAMS 60
Db 1 MKPRARGWRLAALMMLAQAQVSPGRSHQGNRGSGGLEASPRLLSRGPRRLTAMS 60
QY 61 PLFSAGTCVRHGTSSGSAWEPERPASSSTRGAAGLDGKGRDMEAGNHRSGQTNTGTENQ 120
Db 32 PAAAA-----PGSPSVPRPPPPAERPG-----WMEKG-----ACAMG 31
QY 121 TLHVLTYDYLVSAYEVDHREGDYVSHEIMHQRRRAVAVSEVSLHLRLKGRHDFHMDL 180
Db 59 -----EYDLVSAYEVDHREGDYVSHEIMHQRRRAVAVSEVSLHLRLKGRHDFHMDL 112
QY 181 RTSSSLVAPGFIQTGKTGTSVQTLPPEDFCFYOGSLRSHRNSPSHGKCEGSTRTL 240
Db 113 RTSSSLVAPGFIQTGKTGTSVQTLPPEDFCFYOGSLRSHRNS-SVALSTCGLSGMI 171
QY 241 KLCNSQKCPRDSVDFRAAQCAEHNSRRFRGR-----HYKMKPYTQVEA-DLCKLYCI 291
Db 172 R-----TEADYFLRPLPSHLISWKL-GRAAQSSPSHVLTKRSTEPHAPGASEVLVT 222
QY 292 AEGFDFFFS--LSNKVKDGTPCSEDSRNVCI DGCILSVSTSAHMPQPKEDLFI LPDE 349
Db 223 SRTWELAHQPLHSSDLRLGLP--QKHFC-----GRKKYMPQPKEDLFI LPDE 270
QY 350 YKSCLRHKRSLRSHRNEELNVETLVVVDKKMOMNHGHEINTTYVLTILNVSALFKD-- 407
Db 271 YKSCLRHKRSLRSHRNEELNVETLVVVDKKMOMNHGHEINTTYVLTILNVSALFKDGT 330
QY 408 -----GLMGKDGTGRHDAIILLTGLD 427
Db 331 IGGNINIAIVGLILLEDEQPLVISHHADHTLSSFCQWQSGLMGKDGTGRHDAIILLTGLD 390
QY 428 ICSWKNEPCDTLGFAPISGMSKYRSCCTINEDTGLGIAFTIAHESGHNFGMIHDGEGNMC 487
Db 391 ICSWKNEPCDTLGFAPISGMSKYRSCCTINEDTGLGIAFTIAHESGHNFGMIHDGEGNMC 450
QY 488 KKEGNI MSPTLA GRNGVFSWSPCSRQYLHKFLSTAQ 524
Db 451 KKEGNI MSPTLA GRNGVFSWSPCSRQYLHKFLRSVK 487

RESULT 5
US-09-963-791-2
Sequence 2, Application US/09963791
Patent No. 6649399
GENERAL INFORMATION:
APPLICANT: Donoho, Gregory
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Friedrich, Glenn
APPLICANT: Scoville, John
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6649399e1 Human Proteases and Polynucleotides Encoding the San
FILE REFERENCE: LEX-0105-USA
CURRENT APPLICATION NUMBER: US/09/963,791
CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: US 60/169,769

RESULT 7
US-09-981-953A-4
; Sequence 4, Application US/09981953A
; Patent No. 6689599
; GENERAL INFORMATION:
; APPLICANT: RACIE, LISA A.
; APPLICANT: TWINE, NATALIE C.
; APPLICANT: AGOSTINO, MICHAEL J.
; APPLICANT: WOLFMAN, NEIL
; APPLICANT: MORRIS, ELISABETH A.
; TITLE OF INVENTION: NOVEL AGGREGANASE MOLECULES
; FILE REFERENCE: 08702.0075-00000
; CURRENT APPLICATION NUMBER: US/09/981,953A
; CURRENT FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/242,317
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1104
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of unknown Organism: Amino acid
; OTHER INFORMATION: sequence of the aggreganase molecule
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1104)
; OTHER INFORMATION: Any amino acid
US-09-981-953A-4

Query Match 23.7%; Score 1243; DB 4; Length 1104;
Best Local Similarity 31.4%; Pred. No. 6.6e-102;
Matches 295; Conservative 133; Mismatches 317; Indels 194; Gaps 24;
QY 84 PASSSTRGAGLDGKGRDMDAGNHRSQGTNTGTENQTLHVLTYQDVLVSAYEVDHGRDYV 143
DB 3 PACQILRWALAL-GLGLMFETVTHAFRSQ-----DEFLSSLSBSYEIAFPTRVDHNGALL 54
QY 144 SHEIMHQRARRAVAVSEVESLHLRLKGRPHDFHMDLRTSSSLVAPGFIVQTLGKTGTS 203
DB 55 AFSPPRRQRGRGTGATASRLFYKVASPSHFLNLNLTSSRLLAGHVSVEYWTREGIAW 114
QY 204 VQTLRPEDFCFYQGLSRHNS-----PSHGKFCBGSTR 238
DB 115 QRAARPH--CLYAGHLQGGQASHVAISTCGGLHGLIVADEEYYLIEPLHGGP--KGS-- 168
QY 239 TLKLCNSQKPRDS---VDFRAAQ-----CAHNSRRFRGRHYKWKPYTQVEADLC 286
DB 169 -----RSPBESGPHVYKRSSLRHPHLDTACGVDEKPMKGRPMWLRLTKRPPAR-- 218
QY 287 KLYCIAEGDFEFSLSNKVXDGTPCSEDSRNVCIDGICELSVSTSAHMPQPKEDLFL 346
DB 219 -----PLGNETERQGP-----GL----- 231
QY 347 PDEYKSCLRHKRSLRSHRNEELNVETLVVVDKMMQNHGHEINITTYVLTILMVSALFK 406
DB 232 -----KRSVSR-----ERYVETLVADKMVMAYHGRDVEQYVLAIMNIVAKLFQ 276
QY 407 DGLMG-----KDG- 414
DB 277 DSSLGSTVNILVTRLILLTEDOPTLEITHHAGKSLDSFCMKQKSI VNHSGHNAIPENG 336
QY 415 TRHDHAILLTGLDICSWMKNEPDTLGFAPISGMSKYSCTINEDTGLAFTIAHESGH 474
DB 337 ANHDTAVLITRYDICIYKKNKPGTGLAPVGMCEBERSCSVNEDIGLATFTIAHEIGH 396
QY 475 NFGMIHDEGNMC---KSEGNIMSPTLAGRNGVFSWSPCSRQYLHKLFLSTAQAICLADQ 531
DB 397 TFGMNHGVDGNSCGARGQDPKALMAAHITMKTNPFWSSCSRDYITTSFLDSGLGLCLNMR 456

QY 532 PKPVKEVYPEKLPBELYDANTQCKWQFGEKAKLCMLDFKKDICKALWCHRIGRKCETKF 591
DB 457 P-PRQDFVYPTVAPGQAYDADEQCRFQHGYSRQCKYG---EVCSELWCSKSNRCITNS 512
QY 592 MPAAEGTTC-GHDM---WCRGGQCVKYGDBGPKPTHGHSWDSWSWSPCSRTGGGVSHRS 647
DB 513 IPAEGTLCQHTHTIDKGCWYKRVCPFGSR-PEGVDGAMGFWTPWGDGRTCCGVSSSS 571
QY 648 RLCTNPKPSHGKFCCEGSTRTLKLCNSQKPRDSVDFRAAQCAEHNSRRFRGRHYKWKPY 707
DB 572 RHCDSPRPTIGKCYCLGERRRHRSCTDCCPQSGDFREYQCSBFDSIFRGKFKWKTY 631
QY 708 TQVEDQDLCKLYCIAEGDFEFSLSNKVXDGTPCSEDSRNVCIDGICERVGCDNLGSDA 767
DB 632 -RGGVYKACSLTCLAEGFNFYTERAAAVDGTPCRPDYDICSVECKYGCDDRVLGSDL 690
QY 768 VEDVCGVCGNNSACTIHRGLYTKHHNTQYHMTIPSGARSIRIYEMNVSTSYISVRN 827
DB 691 REDKCRVCGDGSACETIEGVFSPASPGAGYEDVWVIRKGSVHFIQDNLJSLHALKG 750
QY 828 ALRRYVLNHWTVDMPCRFKSGTTFDYRRSYNEPENLITGPTNETLIVELLFOGRNP 887
DB 751 DQESLLLEGLPPTPQPHRLPLAGTTFQLRQGPQVQSLALGPINASLIVWLTARTELPA 810
QY 888 VAMEYSMPRLGTEKQPPAQPSTYTAIVR-SECSVSCGG 925
DB 811 LRYRFNAP-IARDSLP---YSWHYAPWTKCSAQACAG 844

RESULT 8
US-09-369-364A-5
; Sequence 5, Application US/09369364A
; Patent No. 6391610
; GENERAL INFORMATION:
; APPLICANT: Apte, Suneel
; APPLICANT: Hurskainen, Tiina L.
; APPLICANT: Hirohata, Satoshi
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; FILE REFERENCE: 26473/4007/10-30-00
; CURRENT APPLICATION NUMBER: US/09/369,364A
; CURRENT FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 859
; TYPE: PRT
; ORGANISM: Homo sapiens ADAMTS-6
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (450)
; OTHER INFORMATION: Xaa = L
US-09-369-364A-5

Query Match 22.7%; Score 1188; DB 3; Length 859;
Best Local Similarity 31.4%; Pred. No. 3.7e-97;
Matches 284; Conservative 132; Mismatches 289; Indels 200; Gaps 25;
QY 108 HRSQQTNTGTENQTLHVLTYQDVLVSAYEVDHGRDYVSHIIM--HQRRAV---AVSE 161
DB 22 HSDHRLSSSQSEFLTYLEHYQLTIPRYDONGAFLSFTYKNDKHSRRRSMDPIDPOQA 81
QY 162 VESLHLRLKGRPHDFHMDLRTSSSLVAPGFIVQTLGKTGTSVQTLRPE-----DFCFY 215
DB 82 VSKLFFKLSAYGKHFLNLINTDFVSKFTVEYWGKDG-----PQMKHDFLDNCHY 133
QY 216 QGSLRSHRNSPSHGKFCCEGSTRTLKLCNSQKPRDSVDFRAAQCAE-FNSRRFRGRHYK 274
DB 134 TGYLQDQR-----STTKVALSN-----CVGLHGVATDEDEEYF 166
QY 275 WKPYTQVEADLCKLYCIAEGDFEFSLSNKVXDGT-----CSEDSRNVCIDGICELSV 328
DB 167 IEPLKNTTED-----SKHFSY-----ENGHPHVIYKKSALQQRHLVDHSHCGVSD 211

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QY 329 VSTSAHMPQPPKEDLFILPDEYKSC--LRHKRSLRSHRNEELNVETLVVDKKMOMNH 385
Db 212 FTRSGKPMWLNDTPLFLIHQINNTHTIHRQRSV-----SIERFVETLVVADKMMGYH 266
QY 386 GHENITTYVTLTNVVSALFKDGLMG----- 411
Db 267 GRKDIEHYILSVNIVAKLYRDSLSGNVNIIVARLIVLTEDQPNLEINHADKSLDSFC 326
QY 412 -----KDQ-----TRHDHALLLTGLDISCMKNPECDTLGFAPISGMSCKYRS 453
Db 327 KMQKSILSHQSDGNTIPENGIAHHDNAVLTIRYDICTYKNKPCGTLGLASVAGMCEPERS 386
QY 454 CTINEDTGLGLAFTIAHESGHNFGMHDEGGMCKSEGNIMSPTLAGRNGVFSWSPCSR 513
Db 387 CSINEDIGLGSFTIAHEIVHNFGMNHDIGNSC-----GR----- 422
QY 514 QYLHKFLSTAQAICLADQPKPVKEYKYPEKLPGELYDANTQCKMOPGEAKL CML----- 568
Db 423 -----KVMKQ-----QNYGSSHYCEYQ--SFFLVCLQSRXHH 452
QY 569 DFKDDICKALWCHRIGRKCETKFMPAAEGTICG--HDMCRGGQCYKYGDGPKPTHG 624
Db 453 QLFREVCRELMCLSKSNRCVTNSIPAAEGTLCQTGNIIEKWCYQGDVFPFG-TWPQSIDG 511
QY 625 HNSDWSWSPPCSRTCGGGVSHRSRLCTNPKPSHGKCEGSTRTLKLCNSQKCPRDSYDF 684
Db 512 GWGFWSLMGECSTRICGGGVSSSLRHCDSPAPSEVEKYCLGERKRYRSCNTDPCPLGSRDF 571
QY 685 RAAQCAEHNSRRFRGRHYKWKPYTQVEDQDLCKLYCIAEGFDFFSLSNKKYKDGTPCESD 744
Db 572 REKQCADFDNMPFRGKYNNKPYTGGGVKP-CALNCLAEYNFYTERAPAVIDGTQCNAD 630
QY 745 SRNVCIDGICERVCNDNLGSDAVEVCGVCNGNNSACTIHRGLYTKHHHTNQYHAWTI 804
Db 631 SLDICINGECKHVGCDNIIIGSDAREDRCRVCGGGGTCDAIEGFENDSLPRGGMEVQI 690
QY 805 PSGARSIRIYEMNVSTSYISVRNALRYYLNGHWYDMPGRYKFSCTTDPYRRSYNBPEN 864
Db 691 PRGSVHIEVREVMASKNYIALKSEGGDYIINGAWTIDMPRKPDVAGTAIFYKRPTEBPES 750
QY 865 LIATGPTNETLIVELLFQGRNPGVAMEYSMP--RLGTEKQPPAQPSTWAIVR--SECSVS 921
Db 751 LEALGPTSENLIWVLLQEQNLGIRYKFNVPITRTSGDN--EVGFTWNHQPWSSECSAT 807
QY 922 CGGGR 926
Db 808 CAGGK 812

RESULT 9
US-09-369-364A-7
; Sequence 7, Application US/09369364A
; Patent No. 6391610
; GENERAL INFORMATION:
; APPLICANT: Apte, Suneel
; APPLICANT: Hurskainen, Tiina L.
; APPLICANT: Hirohata, Satoshi
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; FILE REFERENCE: 26473/4007/10-30-00
; CURRENT APPLICATION NUMBER: US/09/369,364A
; CURRENT FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 997
; TYPE: PRT
; ORGANISM: Homo sapiens ADAMTS-7
US-09-369-364A-7

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Query Match	22.5%;	Score 1179;	DB 3;	Length 997;
Best Local Similarity	30.3%;	Pred. No. 3e-96;		
Matches 292;	Conservative 125;	Mismatches 307;	Indels 240;	Gaps 26;

QY	129	DIVSAVEVDHGRDGVSHSEIMHQRRRAVAVSEVESLHLRLKGPFRDHMDLRTSSSLVA	188
Db	44	DIVHPVRVDAGGSFLSYELMWPRALRKRDVSVRRDAPAFYELQYRGRELRFNLTANQHLLA	103
QY	189	PGFIVQTLGKTGTSVQTLPRPEDECFYQGSLSRHSNPSHGG---KFCGSTRTLKLCN	244
Db	104	PGFVSETRRRGGIGRAHIRAHTPACHLLGEV---QDELEGGLAAISACDGLKGVFQJLSN	160
QY	245	SQKC--PRDSVDFRAAQCAEH-----NSRRFRGHHYKWKPYT---QVEADLCKLYCIAE	293
Db	161	BDYFIEPLDSAPARPGHAQPHVYKQAPERLQAQGDSSAPSTCGVQVPEL-----	212
QY	294	GFDFFFSLSNKVKDGTPCSSEDSRNVCIDIGICELSVSTSAHMPQPKEDLFI LPDEYXSC	353
Db	213	-----ESRR-----ERWEQR	222
QY	354	LHKRSLRS--HR---NEELNVETLVVDKMMQNHENITTYVLTILNMVSALFKDGL	409
Db	223	QQWRPRRLRLRHQRSVSKEKWCETLVVADAKMEYHQPOVESYVLTIMNVAGLFHDS	282
QY	410	MGR-----DGT-----RHDHAILLT	424
Db	283	IGNPIHITIVRLVLEDEEEDLKITHADNTLKSFCWKQKSINMKGDAPHLHDTAILLT	342
QY	425	GLDICSWKNEPCDTLGFAPISGMSKYRSCCTINEDTGLGLAFTIAHESGHNFGMIHDEG	484
Db	343	RDLCAAMNRPCEITGLSHVAGMCOPHRSCSINETGLPLAFTVAHELHGSFGIOHDSG	402
QY	485	NMCKK--SEGNI MSPTLA GRNVFSWSPCSRQYLHKFLSTAQICLADQP-KPYKEYKP	541
Db	403	NDCEPVGKRPFI MSPQLLYDAAPL TWSRCSRQYITRFLDRGWLCLDDPRAKDIID--FP	460
QY	542	EKLPGELYDANTQCKMQFGEKAKLCMLDFKDKICALMCHRIGRKECTKMPAEGTICG	601
Db	461	SVPBGVLVDVSHQCRLQYGAYSFC--EDMDNVCHTLWC-SVGTTCHSKLDAADVGTFCG	517
QY	602	HDMWCRGGQCVKYGDEGPKPTHGHWSDWSSWSPCSRTOCGGVSHRSRLCTNPKPSHGKF	661
Db	518	ENKMCLSGECVYVGFPR-PEAVDGGWSGMSAWSICSRSCGMGVQSAERQCTOPTPKYKGRY	576
QY	662	CEGSTRTLKLCNSQKCPRDSVDFRAAQCAEHNSRRFRGRHYKWKYTYTOVEDODLCKLYCI	721
Db	577	CVGERKRFRLCNLOACPRAGRPSFRHVQCSHFDMMLYKGQLHTWVYV--VNDVNPCELHCR	634
QY	722	AEGFDFFFSLSNKVKDGTPCSE--DSRNVCIDIGICERVGCDNVLSDAVEDVCGVCNGN	779
Db	635	PANEYFAKULRDACVDGTPTCYQVPRASRDLCTINGICKNVGCDFEISGAMEDRCGVCHGNG	694
QY	780	SACTIHRGLYTKHHHTNOYIYHMTIPSGARSIRIYEMNVSTSYISVNA-LRRIYLNHGW	838
Db	695	STCHTVSGTBEAEGLG-YVDVGLIPAGAREIKIQEVAEAPANFLALRSEDEPEKYFILNGW	753
QY	839	TVDWPGRYKSGSTTFDYRRSYNEBENLIATGPNE-----	873
Db	754	TIQWNGDIQVAGTTFTTYARRGNW-ENLTPSPGTYKEPVMIOVPASRGPGGSGRGVPRPST	812
QY	874	-----	873
Db	813	LHGRSRPGGVSPGSVTEPGESEBPPAAASTSVPSLKWPNLVAAVHRGGWGQAPLIGIGW	872
QY	874	-----TLIVELLFOGRNPGVAMEYSMPRI--GTEKOPPAOPSYTWAIVRSECSVS	921
Db	873	RRLVLMMGPRLPTQLLFQESNPGVHYEYTIHREAGGHDEVPR--FVFSWHYGPWTIKCTVT	930
QY	922	CGGG	925
Db	931	CGRG	934

RESULT 10
US-09-369-364A-17
; Sequence 17, Application US/09369364A
; Patent No. 6391610


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Db 416 YTNPMWMSKSCRKYTEFLDTGYGECLENPES-RPYPLPVOLPGILYNVNXOELIFGP 474
QY 562 KAKLCMLDPFKKDICKALMCHRIG---RKCETKMPAEGTICGHDMWCRGGQCVKYGDEG 618
Db 475 GSQVCPYMMQ---CRRLMCNNVGVHKGCRITQHTPWADGTCEBEGKHCKXGFCVPKEMDV 531
QY 619 PKPTHGWSWMSWSPCSRTCGGGVSHRSRLCTNPKPSHGKCEGSTRTLKLCNSQKCP 678
Db 532 P-VTDGSWGSWSPFGTCSRTCGGGIXTAIRECNRPBPKNGKCYCVRMRMKFKSCNTEPCL 590
QY 679 RDSVDFRAAQCAEHNSRRFRGRHY-----KMKP-YTQVEDDQLCKLYCIAEGFDF 728
Db 591 KQKRDFRDEQCA-----HFDGKHFNINGLLPNVVRWVPKYSGLMKDRCKLFCRVAAGNTAY 645
QY 729 FSLSNKVKGDTPCSESDSRNVCIDGICERVGCDNVLGSDAVEDVCGVCNGNNSACTIHRGL 788
Db 646 YQLRDRVIDGTPCGQDTNDICVQGLCRQAGCDHVLNSKARRDKCGVCGGDNSSCKTVAGT 705
QY 789 YTKHHTNOYYHMTIPSGARSIRIEMNVS-----TSYISVRNALRRYYLNGHWTVDWP 843
Db 706 FNTVHY--GYNTVVRIPAGATNIDVRQHSFSGETDDNLTALSSSKGEFLNGNFVVTMA 763
QY 844 GR-YKFSGTFDYRRSYNEPENLIATGPTNETLIVELLFOGR--NPGVAMEYSMPRLGTE 900
Db 764 KREIRIGNAVVEYSGETAVERINSTRIQELLQVLSVGLKYNPDVRYSEFNIP---IE 820
QY 901 KQPP-----AQPST----- 909
Db 821 DKPQQFYWNHSGFWQACSKPCQGERKRLVCTRESQDLTVSDQRCDRLPQPGHITPCGT 880
QY 910 ----TWAIV-RSECSVSCG-GGRCLPV 930
Db 881 GCDLRMHVASRSECSAQCGLGRTLDI 907

RESULT 12
US-09-321-987B-4
; Sequence 4, Application US/09321987B
; Patent No. 6730820
; GENERAL INFORMATION:
; APPLICANT: Kimble, Judith E
; APPLICANT: Bleiloch, Robert H
; TITLE OF INVENTION: Agent and Method for Modulating Cell Migration
; FILE REFERENCE: 960296,95386
; CURRENT APPLICATION NUMBER: US/09/321,987B
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,170
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 60/129,023
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 950
; TYPE: PRT
; ORGANISM: Murine
US-09-321-987B-4

Query Match 19.5%; Score 1022.5; DB 4; Length 950;
Best Local Similarity 30.6%; Pred. No. 2,9e-82;
Matches 266; Conservative 99; Mismatches 319; Indels 185; Gaps 32;

QY 167 LRLKGRHDFHMDLRTSSSLVAPGFIVQTLGKTGKSVQTLPPED---FCFYQGLRSHR 223
Db 64 LRLDAFGQQLHLKLPDSGFLAPGFTLQTVGRSPGSEAQHLDPGTDLAHCFYSGTVNGD- 122
QY 224 NSPSHGKFCGSGSTRTLKLCNSQKCPRDSVDFRAAQCAEHNSRRFRGRHYKWKPYTQVEA 283
Db 123 -----PGSAAALSLCEG-----VRGAFY----- 140
QY 284 DLCKLYCIAEGFDFEFS-----LSNKVKDGTPCSEDSRN-----VCIDG 322
Db 141 -----LOGEEFFIQLPAPGVATERLAPAVVEEBSARQPHILRRRRRSGGAKC--G 190
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QY 323 ICELSVSNPSAHMPQ-----PEKEDLFILPDEYKSLRHKRSLRSHRNEELN 370
Db 191 VMDEDELPTSDSRPESQONRNQWPVRDPTPQDAG--KPSGPGSIRKKRFV-----SSPRY 243
QY 371 VETLVVVDKMMQNHGHNITTYVLTILNMVSALFK----- 406
Db 244 VETMLVAQDSMADFHG--SLKHLYLTLSVAARFYKHPISIRNSISLVVVKILVIEEQKG 302
QY 407 -----DGLMKDQTRHDAILLTGLDICSWKNEPDDTLGFAPIS 445
Db 303 PEVTSNALTLRNFCCNMQKQHNPSDRDPEHYDTAILFTRODLG--SHTCDTLGMADV 360
QY 446 GMCSKYRSGCTINEDTGLAFTIAHESGHNFGMIHDEGNMCKKSEG-----NIMSPTLA 500
Db 361 TVCDPSRSGSVIEDDGLQAAFTTAHELGHVFNMPHD--DAKHGASLNGVTGDSHLMASMLS 419
QY 501 GRNGVFSWSPCSRQYLHKFLLSTAQALCLADQPKPVKEKYKPEKLPGELYDANTQCKMWF 560
Db 420 SLDSHQPSWSPCSAYMTWTSFLDNGHECLMD--KPQNPITKLPSDLPGTLYDANRQCF 477
QY 561 EKAKLCMLDPFKKDICKALMCHRIGK-----CETKMPAEGTICGHDMWCRGGQCVKY 615
Db 478 ESKHC--PDAASTCTTIMC--TGTSGLLVCCQTKHFPWADGTSCGEGKCVSGKCVNKT 533
QY 616 D--EGPKPTHGWSWMSWSPCSRTCGGGVSHRSRLCTNPKPSHGKFCGSTRTLKLCN 673
Db 534 DMKHPATVHGSGWGPWGWGDCSRITCGGQVQYTMRECDNPVPKNGKCYCEGKRVRYRSCN 593
QY 674 SQKCP-RDSVDFRAAQCAEHN--SRFRGRH--YKMKP-YTQVEDDQLCKLYCIAEGFDF 727
Db 594 IEDCPDNNGKTFREBQCAHNEFSAKSGFNEPTVEWTPKYAGVSPKDRCKLTCEAKGIGY 653
QY 728 FFLSNKVKGDTPCSESDSRNVCIDGICERVGCDNVLGSDAVEDVCGVCNGNNSACTIHRG 787
Db 654 FFLQPKVVDGTPCSPDSTSVCGQCYKAGCDRIIDSKKKFKDKCGVCGNGSTCKKMSG 713
QY 788 LYTGHHTNOYYH-MVTIPSGARSIRIEMNV-----STYISVRNALRRYYLNGHWTVD 841
Db 714 IYTS---TRPGYHDIYTIIPAGATNIEYKHRNQGRSRRNGSFLAIRADGTIYILNGNFTLS 770
QY 842 WPKR-YKFSGTFDYRRSYNEPENLIATGPTNETLIVELLFOGR--NPGVAMEYSMPRLG 898
Db 771 TLEQDLTYKGTVLRYSGSSAALERISFPLKEPLTIQVLMVGHALRPKIKFTYFMK-- 828
QY 899 TEKQPPAQPST-WAIVR-SECSVSCGG 925
Db 829 KTESFNALPTFSEWVIEBWEGECSKTCGSG 857

RESULT 13
US-09-981-953A-2
; Sequence 2, Application US/09981953A
; Patent No. 6689599
; GENERAL INFORMATION:
; APPLICANT: RACIE, LISA A.
; APPLICANT: TWINE, NATALIE C.
; APPLICANT: AGOSTINO, MICHAEL J.
; APPLICANT: WOLFMAN, NEIL
; APPLICANT: MORRIS, ELISABETH A.
; TITLE OF INVENTION: NOVEL AGGREGANASE MOLECULES
; FILE REFERENCE: 08702.0075-00000
; CURRENT APPLICATION NUMBER: US/09/981,953A
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/242,317
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
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OTHER INFORMATION: Description of Unknown Organism: Amino acid
OTHER INFORMATION: Sequence of the aggreganase molecule
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (200)
OTHER INFORMATION: Any amino acid
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (214)
OTHER INFORMATION: Any amino acid
US-09-981-953A-2

Query Match 19.5%; Score 1022; DB 4; Length 770;
Best Local Similarity 37.8%; Pred. No. 2.3e-82;
Matches 213; Conservative 91; Mismatches 207; Indels 52; Gaps 16;

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Db 41 QKIVNHSGHGN-----ALPENGV-----ANHDTAVLITRYDICIYKNKPCG 82
QY 438 TLGFAPISGMSKYSRCTINEDTGLAFTIAHESGHNFGMIHDEGNMC---KSEGN 494
Db 83 TLGLAPVGMCEKERSCSVNEDIGLATAFTIAHEIGHTFGMNHGVSNSCGARGDPAKL 142
QY 495 MSPTLAGRNGVFSWSPCSRQYLHKFLSTAQAICLADQPKVKEYKYPEKLPGELYDANTQ 554
Db 143 MAAHITMKTNPFWSSCSRDIYITFLDSGPG-ALPEQAPQGTGLCVPDSGTG----PSLR 197
QY 555 CK-----WQFGEKAKLCMLDFKKDICKALWCHRIGRKCETKEMPAEGTIC-GHDM-- 604
Db 198 CRXAMPPLSAW-----SQIASVXI-REVCESELWCLSKSNRCITNSIPAEGTLCQTHITDK 251
QY 605 -WCRGGQCVKYGDEGPKPTHGNSDMSWSPCSRTCGGGVSHRSRLCTNPKPSHGKFCF 663
Db 252 GWCYKRVCFPGSR-PBGVDGAWPMTWGDCCSRTCCGGVSSSRHCDSPRTIGGKYCL 310
QY 664 GSTRTKLCSQKCPRDSVDFRAACAENHSRRPRGRHYKWKPYTQVEDQDLCKLYCIAE 723
Db 311 GERRRHRSCTDCCPFGSQDFREVQCSEFDSIPPRGKPYKWKTY-RGGGVKACSLTCLAE 369
QY 724 GPDFPFSLSNKYKDGTPCSEDSRNVCIDGICERVGCDNVLSDAVEDVCGVCGNNSACT 783
Db 370 GFNFYTERAAAVVDGTPCRPDYIDICVSGECKHVGCIDRVLSDLREDKCRVCGGDSACE 429
QY 784 IHRGLYTKHHHTNOYHAMVTIPSGARSIRIYEMNVSTYISVRNALRRYYLNGHWTVDWP 843
Db 430 TIEGVFSPASPGAGYEDVWVIFPKGSVHFIQDLNLSLHALKGDQESLLLEGLPETPOP 489
QY 844 GRYKFSGTFDYRRSYNEPENLIATGPTNETLIVELLFOGRNPGVAWEYSMPRLGTEKOP 903
Db 490 HRLPLAGTTFOLRQGPDDQVQSLBALGPINASLIWVLARTELPALRYRFNAP-IARDSLP 548
QY 904 PAQPSYTWAIVR-SECSVSCGGG 925
Db 549 P----YSWHYAPWTKCSAQACAGG 567

RESULT 14
US-09-369-364A-15
Sequence 15, Application US/09369364A
Patent No. 6391610
GENERAL INFORMATION:
APPLICANT: Apte, Suneel
APPLICANT: Hurskainen, Taina L.
APPLICANT: Hirohata, Satoshi
TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
FILE REFERENCE: 26473/4007/10-30-00
CURRENT APPLICATION NUMBER: US/09/369,364A
CURRENT FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 874

TYPE: PRT
ORGANISM: Mus musculus ADAMTS-9
US-09-369-364A-15

Query Match 18.9%; Score 991; DB 3; Length 874;
Best Local Similarity 34.2%; Pred. No. 1.7e-79;
Matches 215; Conservative 107; Mismatches 210; Indels 96; Gaps 20;

QY 371 VETLVVDDKKMNHGHENITTYVLTILNVSALEKDGMLGK----- 412
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QY 413 -----DGRHDHAILLTGLDICSWKNEPCDTLGFAPISGMC 448
Db 193 PYINFNAQTTLKNFCQWQHSKNYLGIGIHDPTAVLVTREDICR-AQDKCDTLGLAELGTIC 251
QY 449 SKYRSTINEDTGLAFTIAHESGHNFGMIHDEGNMC---KSEGNMPTLAGRNG 504
Db 252 DPYRSCSISEDGSLSTAFTIAHBLGHVFNMPHD-DSNCKKEGVKSPQHVMAPTLNFYTN 310
QY 505 VFSWSPCSRQYLHKFLSTAQAICLADQPKVKEYKYPEKLPGELYDANTQCKWQFGEKAK 564
Db 311 PMWMSKSRKITEFLDTGYGBCLLNBPAS-RTYPLPSQLPGLLYNVNKQCELIIFGPGSQ 369
QY 565 LCMLEFKKDICKALWCHRI---RKCETKEMPAEGTICGHDMWCRGGQCVKYGDEGPKP 621
Db 370 VCPYMQ---CRLWCNNVDAHKGCKTQHTPWADGTCEBPGHKCFGVCPREMEGP-A 425
QY 622 THGWSWDSWSPCSRTCGGGVSHRSRLCTNPKPSHGKFCGSTRITKLCSQKCPRDS 681
Db 426 IDGSWGWMSHGTCSTRTCGGGIKTAIRECNBEPKNGGKYCVGRMKFKSCNTEPCMOK 485
QY 682 VDFRAAQCAENHSRRPRGRHY-----KMKP-YTQVEDQDLCKLYCIAEFDFFFSL 731
Db 486 RDFREBQCA-----HPDGKHFNINGLLPSVYRFPKYSGILMKDRCKLFCRYAGNTAYYQL 540
QY 732 SNKYKDGTPCSEDSRNVCIDGICERVGCDNVLSDAVEDVCGVCGNNSACTIHRGLYTK 791
Db 541 RDRVIDGTPCGODTNDICVQGLCRQAGCDHILNSKVRKDKCGICGGDNSSCTVAGTFNT 600
QY 792 HHHTNOYHAMVTIPSGARSIRIYEMNVSTYISVRNALRRYYLNGHWTVDWPGR- 845
Db 601 VHY--GYNTVIRIPAGATSIDVRQHSFSGKSEDDNYLALSNSKEFFLNGDFVVSMSKRE 658
QY 846 YKFSGTFDYRRSYNEPENLIATGPTNETLIVELLFOGR--NPGVAWEYSMPRLGTEKOP 903
Db 659 VRVGSVIVISGSDNVCERLNTDRIEELLQVLSVGKLYNPDRVYSFNIP---IEDKP 715
QY 904 PAQPSY-----TWAIVRSECSVSCGGG 926
Db 716 --QQFYWNSHGPW---QACSKPCQGER 737

RESULT 15
US-09-130-491-2
Sequence 2, Application US/09130491
Patent No. 6416974
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
APPLICANT: Goodearl, Andrew D.J.
TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND TANGO-83
FILE REFERENCE: 09404/041001
CURRENT APPLICATION NUMBER: US/09/130,491
CURRENT FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: US 60/058,108
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: US 60/054,961
EARLIER FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 967
TYPE: PRT

GenCore version 5.1.6
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OM protein - protein search, using sw model

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	5236	100.0	952	US-09-981-151A-8	Sequence 8, Appli
2	5110	97.6	986	US-09-981-151A-2	Sequence 2, Appli
3	4103.5	78.4	791	US-09-981-151A-4	Sequence 4, Appli
4	3858.5	73.7	1224	US-10-275-107-51	Sequence 51, Appl
5	3846.5	73.5	1224	US-10-217-774-4	Sequence 4, Appli
6	3846.5	73.5	1224	US-10-296-616-2	Sequence 2, Appli
7	3846.5	73.5	1224	US-10-804-457-4	Sequence 4, Appli
8	3365	64.3	856	US-09-981-151A-6	Sequence 6, Appli
9	3286	62.8	1236	US-10-399-645-4	Sequence 4, Appli
10	2435.5	46.5	1221	US-10-240-545A-2	Sequence 2, Appli
11	2434.5	46.5	1082	US-10-363-937-17	Sequence 17, Appli

12	2434.5	46.5	1221	15	US-10-354-983-2	Sequence 2, Appli
13	2430	46.4	1365	15	US-10-120-801-48	Sequence 48, Appl
14	2411.5	46.1	1071	15	US-10-354-983-4	Sequence 4, Appli
15	2408	46.0	1081	15	US-10-120-801-46	Sequence 46, Appl
16	2408	46.0	1081	16	US-10-391-364-87	Sequence 87, Appl
17	2364	45.1	1162	15	US-10-161-493-124	Sequence 124, App
18	2265	43.3	862	14	US-10-226-560-2	Sequence 2, Appli
19	2265	43.3	862	18	US-10-990-935-2	Sequence 2, Appli
20	2255	43.1	914	15	US-10-188-186-132	Sequence 132, App
21	2247.5	42.9	919	15	US-10-188-186-130	Sequence 130, App
22	2196.5	41.9	934	15	US-10-275-107-53	Sequence 53, Appl
23	2079.5	39.7	1123	15	US-10-120-801-45	Sequence 45, Appl
24	1559	29.8	661	15	US-10-354-983-8	Sequence 8, Appli
25	1543.5	29.5	491	13	US-10-217-774-2	Sequence 2, Appli
26	1543.5	29.5	491	17	US-10-804-457-2	Sequence 2, Appli
27	1391	26.6	959	9	US-09-788-043C-1	Sequence 1, Appli
28	1390	26.5	908	9	US-09-963-791-2	Sequence 2, Appli
29	1390	26.5	908	15	US-10-419-276-2	Sequence 2, Appli
30	1390	26.5	908	20	US-11-027-743-2	Sequence 6, Appli
31	1380.5	26.4	1120	15	US-10-467-042-6	Sequence 2, Appli
32	1380.5	26.4	1120	20	US-11-046-868-6	Sequence 6, Appli
33	1376	26.3	684	14	US-10-103-377C-2	Sequence 2, Appli
34	1342	25.6	353	15	US-10-161-493-130	Sequence 130, App
35	1342	25.6	353	15	US-10-161-493-134	Sequence 134, App
36	1339	25.6	353	15	US-10-161-493-128	Sequence 128, App
37	1332	25.4	349	15	US-10-161-493-126	Sequence 126, App
38	1332	25.4	353	15	US-10-161-493-132	Sequence 132, App
39	1319	25.2	757	9	US-09-963-791-24	Sequence 24, Appl
40	1319	25.2	757	15	US-10-419-276-24	Sequence 24, Appl
41	1319	25.2	757	20	US-11-027-743-24	Sequence 24, Appl
42	1257	24.0	1690	9	US-09-788-043C-5	Sequence 5, Appli
43	1246	23.8	1686	15	US-10-386-414-2	Sequence 2, Appli
44	1243	23.7	1044	9	US-09-858-081-9	Sequence 9, Appli
45	1242	23.7	1103	15	US-10-275-107-50	Sequence 50, Appl

ALIGNMENTS

RESULT 1
US-09-981-151A-8
; Sequence 8, Application US/09981151A
; Publication No. US20030212256A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Gerlach, Valerie
; APPLICANT: MacDougall, John R
; APPLICANT: Malysankar, Muriel M
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A
; APPLICANT: Stone, David J
; APPLICANT: Gunther, Erik
; APPLICANT: Ellerman, Karen
; APPLICANT: Shimkets, Richard A
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Guo, Xiaojia
; APPLICANT: Patturajan, Meera
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Burgess, Catherine E
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Gangolli, Esma A
; APPLICANT: Fernandes, Elma R
; APPLICANT: Gorman, Linda
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-168
; CURRENT APPLICATION NUMBER: US/09/981,151A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 60/241,040
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,058

; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,063
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,243
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/242,152
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/242,482
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,611
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,612
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,880
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/242,881
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 952
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-981-151A-8

Query Match 100.0%; Score 5236; DB 10; Length 952;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 952; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKPRARGWRLAALMLLAQVAEQVSPGRSHQGNRGSGQLEASPPRLLSRGPRLTAMS 60
DB 1 MKPRARGWRLAALMLLAQVAEQVSPGRSHQGNRGSGQLEASPPRLLSRGPRLTAMS 60
QY 61 PLFSAGTCVRHGTSSGSAWBERPASSSTRGAAGLDGKGRDMEAGNHRSQQTNTGTENQ 120
DB 61 PLFSAGTCVRHGTSSGSAWBERPASSSTRGAAGLDGKGRDMEAGNHRSQQTNTGTENQ 120
QY 121 TLHVLTYQDLVSAVEVDHGRDVSHEIMHQRRAVAVSEVESLHLRLKGRHDFHMDL 180
DB 121 TLHVLTYQDLVSAVEVDHGRDVSHEIMHQRRAVAVSEVESLHLRLKGRHDFHMDL 180
QY 181 RTSSSLVAPGFIVQTLGKTGTSVQTLPPEDFCFYQGLSRHRNSPSHGKFCGSTRTL 240
DB 181 RTSSSLVAPGFIVQTLGKTGTSVQTLPPEDFCFYQGLSRHRNSPSHGKFCGSTRTL 240
QY 241 KLCNSQKCPRDSVDFRAAQCAEHNSRRFRGRHYKWKPYTOVEADLCKLYCIAEGFDFPFS 300
DB 241 KLCNSQKCPRDSVDFRAAQCAEHNSRRFRGRHYKWKPYTOVEADLCKLYCIAEGFDFPFS 300
QY 301 LSNKVKDGTPECSSEDSRNVCIDGICELSVSTSAHMPQPPKEDLFLPDEYKSCLRHKRSL 360
DB 301 LSNKVKDGTPECSSEDSRNVCIDGICELSVSTSAHMPQPPKEDLFLPDEYKSCLRHKRSL 360
QY 361 LRSHRNEELNVEVLVVVDKMMQNHGENITTYVLTILNVYSALFKDGLMGKDGTRHDHA 420
DB 361 LRSHRNEELNVEVLVVVDKMMQNHGENITTYVLTILNVYSALFKDGLMGKDGTRHDHA 420
QY 421 ILLTGLDICSWKNEPCDTLGFAPISGMSKYRSCCTINEDTGLAFTIAHESGHNFMIH 480
DB 421 ILLTGLDICSWKNEPCDTLGFAPISGMSKYRSCCTINEDTGLAFTIAHESGHNFMIH 480
QY 481 DGEGNMCKSEGNIMSPITLAGRNVFWSWPSRQYLHKFLSTAQAICLADQPKVKEYKY 540
DB 481 DGEGNMCKSEGNIMSPITLAGRNVFWSWPSRQYLHKFLSTAQAICLADQPKVKEYKY 540
QY 541 PEKLPGELEYDANTQCKWQFGEKAKLCMLDFKKDICKALWCHIRIGKCEYKMPAAEGTIC 600
DB 541 PEKLPGELEYDANTQCKWQFGEKAKLCMLDFKKDICKALWCHIRIGKCEYKMPAAEGTIC 600
QY 601 GHDMWCRGGCCVKYGDGEPKPTHGHWSDMSWSPCSRTCGGGVSHRSRLCTNPKPSHGK 660
DB 601 GHDMWCRGGCCVKYGDGEPKPTHGHWSDMSWSPCSRTCGGGVSHRSRLCTNPKPSHGK 660

QY 661 FCEGSTRTLKLCNSQKCPRDSVDFRAAQCAEHNSRRFRGRHYKWKPYTOVEDQDLCKLYC 720
DB 661 FCEGSTRTLKLCNSQKCPRDSVDFRAAQCAEHNSRRFRGRHYKWKPYTOVEDQDLCKLYC 720
QY 721 IAEGFDFEFLSNKVKDGTPECSSEDSRNVCIDGICERVCGDNVLGSDADEVCGVCNGNS 780
DB 721 IAEGFDFEFLSNKVKDGTPECSSEDSRNVCIDGICERVCGDNVLGSDADEVCGVCNGNS 780
QY 781 ACTIHRGLYTKHHTNTQYHMTVTPSGARSIRIYEMNVSYSISVRNALRRYYLNGHWTV 840
DB 781 ACTIHRGLYTKHHTNTQYHMTVTPSGARSIRIYEMNVSYSISVRNALRRYYLNGHWTV 840
QY 841 DWPGRYKFSGTTFDYRRSYNEPENLITATGPTNETLIYELLFOGRNPGVAWEYSMPRLGTE 900
DB 841 DWPGRYKFSGTTFDYRRSYNEPENLITATGPTNETLIYELLFOGRNPGVAWEYSMPRLGTE 900
QY 901 KQPPAQPSTYTWAIVRSEGSVSCGGRCPLVLLLEAACPSTATAYIALAFLES 952
DB 901 KQPPAQPSTYTWAIVRSEGSVSCGGRCPLVLLLEAACPSTATAYIALAFLES 952

RESULT 2
US-09-981-151A-2
; Sequence 2, Application US/09981151A
; Publication No. US20030212256A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Gerlach, Valerie
; APPLICANT: MacDougall, John R
; APPLICANT: Malyanakar, Muriel M
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A
; APPLICANT: Stone, David J
; APPLICANT: Gunther, Erik
; APPLICANT: Ellerman, Karen
; APPLICANT: Shinkets, Richard A
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Guo, Xiaojia
; APPLICANT: Patuturajan, Meera
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Burgess, Catherine E
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Gangolli, Esha A
; APPLICANT: Fernandes, Elma R
; APPLICANT: Gorman, Linda
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-168
; CURRENT APPLICATION NUMBER: US/09/981,151A
; PRIOR FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 60/241,040
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,058
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,063
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,243
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/242,152
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/242,482
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,611
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,880
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/242,881
; PRIOR FILING DATE: 2000-10-24

Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 986
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (283)
; OTHER INFORMATION: wherein Xaa is any amino acid.
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (792)
; OTHER INFORMATION: wherein Xaa is any amino acid.
US-09-981-151A-2

Query Match 97.6%; Score 5110; DB 10; Length 986;
Best Local Similarity 94.6%; Pred. No. 0;
Matches 940; Conservative 1; Mismatches 3; Indels 50; Gaps 4;

QY 1 MKPRARGWGLAALMMLAQVAEVSPPGRSHQRNRSQGLEASPPRLLSRGPRLLTAMS 60
1 MKPRARGWGLAALMMLAQVAEVSPPGRSHQRNRSQGLEASPPRLLSRGPRLLTAMS 60
QY 61 PLFSAGTCVRHGTSGSASWEPEPPASSSTRGAAGLDGKGRDMDAAGNHRSSQQTNTGTENQ 120
61 PLFSAGTCVRHGTSGSASWEPEPPASSSTRGAAGLDGKGRDMDAAGNHRSSQQTNTGTENQ 120
Db 61 PLFSAGTCVRHGTSGSASWEPEPPASSSTRGAAGLDGKGRDMDAAGNHRSSQQTNTGTENQ 120
QY 121 TLHVLTYQYDLVSAVEVDHGRDYVSHIIMHQRRAVAVSEVESLHLRLKGPRLDFHMDL 180
121 TLHVLTYQYDLVSAVEVDHGRDYVSHIIMHQRRAVAVSEVESLHLRLKGPRLDFHMDL 180
Db 121 TLHVLTYQYDLVSAVEVDHGRDYVSHIIMHQRRAVAVSEVESLHLRLKGPRLDFHMDL 180
QY 181 RTSSSLVAPGFIVQTLGKTGTSVQTLPEDFCFYQGLSRSHRNSPSHGKFCGSTRTL 240
181 RTSSSLVAPGFIVQTLGKTGTSVQTLPEDFCFYQGLSRSHRNSPSHGKFCGSTRTL 240
Db 181 RTSSSLVAPGFIVQTLGKTGTSVQTLPEDFCFYQGLSRSHRNSPSHGKFCGSTRTL 240
QY 241 KLCNSQKCPRDSYDFRAAQAENHSRRFRGRHYKWKPYTQVEADLCKLYCIAEGDFEFS 300
241 KLCNSQKCPRDSYDFRAAQAENHSRRFRGRHYKWKPYTQVEADLCKLYCIAEGDFEFS 300
Db 241 KLCNSQKCPRDSYDFRAAQAENHSRRFRGRHYKWKPYTQVEADLCKLYCIAEGDFEFS 300
QY 301 LSNKYKDGTPCSEDSRNVCIDIGICELSVSTSAHMPQPKEDLFLPDEYKSCLRHKRSL 360
301 LSNKYKDGTPCSEDSRNVCIDIGICELSVSTSAHMPQPKEDLFLPDEYKSCLRHKRSL 360
Db 301 LSNKYKDGTPCSEDSRNVCIDIGICELSVSTSAHMPQPKEDLFLPDEYKSCLRHKRSL 360
QY 361 LRSHRNEELNVELTVVVDKKMMQNHENITTYVLTILNVSALFKD----- 407
361 LRSHRNEELNVELTVVVDKKMMQNHENITTYVLTILNVSALFKD----- 407
Db 361 LRSHRNEELNVELTVVVDKKMMQNHENITTYVLTILNVSALFKD----- 407
QY 408 -----GLMGKDGTRHDHAILLTGLDICSWKNEPCDT 438
408 -----GLMGKDGTRHDHAILLTGLDICSWKNEPCDT 438
Db 421 LILLEDEQPLVISHHADHTLSSFCQWQSGLMGKDGTRHDHAILLTGLDICSWKNEPCDT 480
QY 439 LGFAPISGMSKYRSCCTINEDTGLAFTIAHESGHNFGMIHDEGNNCKKSEGNIMSPT 498
439 LGFAPISGMSKYRSCCTINEDTGLAFTIAHESGHNFGMIHDEGNNCKKSEGNIMSPT 498
Db 481 LGFAPISGMSKYRSCCTINEDTGLAFTIAHESGHNFGMIHDEGNNCKKSEGNIMSPT 540
QY 499 LAGRNGVFSWSPCSRQYLHKFLSTAQAICLADQPKPKYKYPEKLPGLYDANTQCKWQ 558
499 LAGRNGVFSWSPCSRQYLHKFLSTAQAICLADQPKPKYKYPEKLPGLYDANTQCKWQ 558
Db 541 LAGRNGVFSWSPCSRQYLHKFLSTAQAICLADQPKPKYKYPEKLPGLYDANTQCKWQ 600
QY 559 FGEKAKLCMLDFKKDICKALMCHRIGRKCETKMPAAEGTICGHDMWCRGGQCYKYGDEG 618
559 FGEKAKLCMLDFKKDICKALMCHRIGRKCETKMPAAEGTICGHDMWCRGGQCYKYGDEG 618
Db 601 FGEKAKLCMLDFKKDICKALMCHRIGRKCETKMPAAEGTICGHDMWCRGGQCYKYGDEG 660
QY 619 PKPTHGHWSWSPCSRTCGGGVSHRSRLCTNPKPSHGKPCGEGSTRITLKLNSQKCP 678
619 PKPTHGHWSWSPCSRTCGGGVSHRSRLCTNPKPSHGKPCGEGSTRITLKLNSQKCP 678
Db 661 PKPTHGHWSWSPCSRTCGGGVSHRSRLCTNPNPSHGKPCGEGSTRITLKLNSQKCP 720
QY 679 RDSVDFRAAQAENHSRRFRGRHYKWKPYTQVEDODLCKLYCIAEGDFEFSLSNKVKXD 738
679 RDSVDFRAAQAENHSRRFRGRHYKWKPYTQVEDODLCKLYCIAEGDFEFSLSNKVKXD 738
Db 721 RDSVDFRAAQAENHSRRFRGRHYKWKPYTQVEDODLCKLYCIAEGDFEFSLSNKVKXD 774

QY 739 TPCESDSRNVCIDIGICERVGCNVLGSDAVEBVCVCGNNGNSACTIHRGLYTKHHTNOY 798
739 TPCESDSRNVCIDIGICE-XGCDNVLGSDAVEBVCVCGNNGNSACTIHRGLYTKHHTN-H 832
Db 775 TPCESDSRNVCIDIGICE-XGCDNVLGSDAVEBVCVCGNNGNSACTIHRGLYTKHHTN-H 832
QY 799 YHMVTIPSGARSIRIYEMNVSTSYISVRNALRRYYLNGHWTVDWPGRYKFGSGTTFDYRS 858
799 YHMVTIPSGARSIRIYEMNVSTSYISVRNALRRYYLNGHWTVDWPGRYKFGSGTTFDYRS 858
Db 833 YHMVTIPSGARSIRIYEMNVSTSYISVRNALRRYYLNGHWTVDWPGRYKFGSGTTFDYRS 892
QY 859 YNEPENLIATGPTNETLIVELLFQGRNPGVAMEYSMPRLGTEKQPPAQPSTYTWAIVRSEC 918
859 YNEPENLIATGPTNETLIVELLFQGRNPGVAMEYSMPRLGTEKQPPAQPSTYTWAIVRSEC 918
Db 893 YNEPENLIATGPTNETLIVELLFQGRNPGVAMEYSMPRLGTEKQPPAQPSTYTWAIVRSEC 952
QY 919 SVSCGGGRCLPVLLLEAACQPSATAYIALAFLES 952
919 SVSCGGGRCLPVLLLEAACQPSATAYIALAFLES 952
Db 953 SVSCGGGRCLPVLLLEAACQPSATAYIALAFLES 986

RESULT 3
US-09-981-151A-4
; Sequence 4, Application US/09981151A
; Publication No. US20030212256A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Gerlach, Valerie
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Muriel M
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A
; APPLICANT: Stone, David J
; APPLICANT: Gunther, Erik
; APPLICANT: Ellerman, Karen
; APPLICANT: Shimkets, Richard A
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Guo, Xiaojia
; APPLICANT: Paturaian, Meera
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Burgess, Catherine B
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Gangolli, Esha A
; APPLICANT: Fernandes, Elma R
; APPLICANT: Gorman, Linda
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-168
; CURRENT APPLICATION NUMBER: US/09/981,151A
; PRIOR FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 60/241,040
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,058
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,063
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,243
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/242,152
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/242,482
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,611
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,612
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,880
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/242,881
; PRIOR FILING DATE: 2000-10-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 791

TYPE: PRT
ORGANISM: Homo sapiens
US-09-981-151A-4

Query Match 78.4%; Score 4103.5; DB 10; Length 791;

Best Local Similarity 81.2%; Pred. No. 0;
Matches 774; Conservative 9; Mismatches 7; Indels 163; Gaps 8;

QY 1 MKPRARGWGLAALMMLAQAQVSPGRSHQGNRSGQLEASPPRLSRGPRRLTAMS 60
DB 1 MKPRARGWGLAALMMLAQAQVSPGRSHQGNRSGQLEASPPRLSRGPRRLTAMS 60
QY 61 PLFSAGTCVRHGTSGSAWEPPERPASSSTRGAAGLDGKGRDMEAGNHRSQQTNTGTENQ 120
DB 61 PLFSAGTCVRHGTSGSAWEPPERPASSSTRGAAGLDGKGRDMEAGNHRSQQTNTGTENQ 120
QY 121 TLHLVT-QYDILVSAYEVDRGDYVSHEIMHQRRAVAVAVEESLHLRLKGRPHDFHMD 179
DB 121 TLHLVTREYDILVSAYEVDRGDYVSHEIMHQRRAVAVAVEESLHLRLKGRPHDFHMD 180
QY 180 LRTSSSLVAPGFIVQTLGKTGTSVQTLPPEDFCFYQGSLSRHRNSPSHGKFCGEGSTRT 239
DB 181 LRTSSSLVAPGFIVQTLGKTGTSVQTLPPEDFCFYQGSLSRHRNSPSHGKFCGEGSTRT 240
QY 240 LKLCNSQKCPRDSVDFRAAQCAEHNSRRFRGRHYKWKPYTOVEADLCLYCIAEGDFDF 299
DB 241 LKLCNSQKCPRDSVDFRAAQCAEHNSRRFRGRHYKWKPYTOVEADLCLYCIAEGDFDF 300
QY 300 SLSNKKVKGTPCSEDSRSRNVCIDGICELSVSTSAHMPQPKEDLFLPDEYKSLRHKRS 359
DB 301 SLSNKKVKGTPCSEDSRSRNVCIDGICE-----MPQPKEDLFLPDEYKSLRHKRS 351
QY 360 LLRSHRNEELNVETLVVVDKMMQNHENITTYVLTILNVSALFKDGLMGKDGTRHDH 419
DB 352 LLRSHRNEELNVETLVVVDKMMQNHENITTYVLTILNVSALFKDGTIG----- 403
QY 420 AILLTGLDICSWKNEPCDTLGFAPISGMSKYRSCCTINEDTGLAFTIAHESGHNFEMI 479
DB 404 ----- 403
QY 480 HDGEGNMCKSEGNIMSPTLAAGRVFWSWSPCSRQYLHKFLSTAQAICLADQPKVKEYK 539
DB 404 -----GNI-NIAIVG----- 412
QY 540 YPEKLPGEIYDANTQCKWQFGEKAKLCMLDFEKDICKALWCHRIGRKCETKMPAAEGTI 599
DB 413 -----LILDEBQDICKALWCHRIGRKCETKMPAAEGTI 447
QY 600 CGHDMWCRGGQCVKYGDEGPKPTHGMSDMSWSPCSRTCGGGVSHRSRLCTNPKPSHG 659
DB 448 CGHDMWCRGGQCVKYGDEGPKPTHGMSDMSWSPCSRTCGGGVSHRSRLCTNPKPSHG 507
QY 660 KFCGEGSTRTKLKCNQKCPRDSVDFRAAQCAEHNSRRFRGRHYKWKPYTOVEDODLCKLY 719
DB 508 KFCGEGSTRTKLKCNQKCPRDSVDFRAAQCAEHNSRRFRGRHYKWKPYTOVEDODLCKLY 561
QY 720 CIAEGDFPFSLSNKKVKGTPCSEDSRSRNVCIDGICERVGCDNVLGSDAVEDVCGVCGNN 779
DB 562 CIAEGDFPFSLSNKKVKGTPCSEDSRSRNVCIDGICE--GCDNVLGSDAVEDVCGVCGNN 619
QY 780 SACTIHRGLYTKHHHTNOYHMTIPSGARSIRIYEMNVSTSYISVRNALRRYYLNGHWT 839
DB 620 SACTIHRGLYTKHHHTN-YHMTIPSGARSIRIYEMNVSTSYISVRNALRRYYLNGHWT 678
QY 840 VDMWGRYKFSGTTFDYRRSYNEPENLIATGPTNETLIVELLFOGRNPGVAWEYSMPRLGT 899
DB 679 VDMWGRYKFSGTTFDYRRSYNEPENLIATGPTNETLIVELLFOGRNPGVAWEYSMPRLGT 738
QY 900 EKOPPAOPSTYTAIVRSECSVCGGRCPLVLLLEAACQPSATAYIALAFLES 952
DB 739 EKOPPAOPSTYTAIVRSECSVCGGRCPLVLLLEAACQPSATAYIALAFLES 791

RESULT 4

US-10-275-107-51

/ Sequence 51, Application US/10275107

/ Publication No. US20040063107A1

/ GENERAL INFORMATION:

/ APPLICANT: PLOWMAN, GREGORY D.

/ APPLICANT: WHYTE, DAVID

/ APPLICANT: SUDARSANAM, SUCHA

/ APPLICANT: MANNING, GERARD

/ APPLICANT: CAENEPEEL, SEAN R.

/ APPLICANT: PAYNE, VILLA

/ TITLE OF INVENTION: NOVEL PROTEASES

/ FILE REFERENCE: 038602/1479

/ CURRENT APPLICATION NUMBER: US/10/275,107

/ PRIOR FILING DATE: 2003-11-03

/ PRIOR APPLICATION NUMBER: PCT/US01/14431

/ PRIOR FILING DATE: 2001-05-04

/ PRIOR APPLICATION NUMBER: 60/201,879

/ NUMBER OF SEQ ID NOS: 105

/ SOFTWARE: PatentIn Ver. 2.1

/ SEQ ID NO 51

/ LENGTH: 1224

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ US-10-275-107-51

Query Match 73.7%; Score 3858.5; DB 15; Length 1224;
Best Local Similarity 75.6%; Pred. No. 0;
Matches 740; Conservative 24; Mismatches 72; Indels 143; Gaps 13;

QY 1 MKPRARGWGLAALMMLAQAQVSPGRSHQGNRSGQLEASPPRLSRGPRRLTAMS 60
DB 1 MKPRARGWGLAALMMLAQAQVSPGRSHQGNRSGQLEASPPRLSRGPRRLTAMS 60
QY 61 PLFSAGTCVRHGTSGSAWEPPERPASSSTRGAAGLDGKGRDMEAGNHRSQQTNTGTENQ 120
DB 32 PAAAA-----PGSPSVPRPPPAERPG-----WMEKG----- 58
QY 121 TLHLVTQYDILVSAYEVDRGDYVSHEIMHQRRAVAVAVEESLHLRLKGRPHDFHMD 180
DB 59 -----BYDLVSAYEVDRGDYVSHEIMHQRRAVAVAVEESLHLRLKGRPHDFHMD 112
QY 181 RTSSSLVAPGFIVQTLGKTGTSVQTLPPEDFCFYQGSLSRHRNSPSHGKFCGEGSTRT 240
DB 113 RTSSSLVAPGFIVQTLGKTGTSVQTLPPEDFCFYQGSLSRHRNS-SVALSTCQGLSGMI 171
QY 241 KLCNSQKCPRDSVDFRAAQCAEHNSRRFRGR-----HYKWKPYTOVEA-DLCKLYCI 291
DB 172 R-----TEADYFLRPLPSHLWKL-GRAAQGSSPSHVLKYRSTEPHAPGASEVLVT 222
QY 292 AEGFDFEFS--LSNKKVKGTPCSEDSRSRNVCIDGICELSVSTSAHMPQPKEDLFLPDE 349
DB 223 SRTWEIAHQPLHSSDLRLGLP--QKHFC-----GRRKKYMQPKEDLFLPDE 270
QY 350 YKSLRHRKSLRSHRNEELNVETLVVVDKMMQNHENITTYVLTILNVSALFKD-- 407
DB 271 YKSLRHRKSLRSHRNEELNVETLVVVDKMMQNHENITTYVLTILNVSALFKDGT 330
QY 408 -----GLMGKDGTRHDHAILLTGLD 427
DB 331 IGININIAIVGLILDEQPLVISHHADHTLSSFCWQSGLMGKDGTRHDHAILLTGLD 390
QY 428 ICSWKNPECDTLGFAPISGMSKYRSCCTINEDTGLAFTIAHESGHNFEMIHDGEGNMC 487
DB 391 ICSWKNPECDTLGFAPISGMSKYRSCCTINEDTGLAFTIAHESGHNFEMIHDGEGNMC 450
QY 488 KKEGNIMSPTLAAGRVFWSWSPCSRQYLHKFLSTAQAICLADQPKVKEYKYPEKLGE 547
DB 451 KKEGNIMSPTLAAGRVFWSWSPCSRQYLHKFLSTAQAICLADQPKVKEYKYPEKLGE 510
QY 548 LYDANTQCKWQFGEKAKLCMLDFEKDICKALWCHRIGRKCETKMPAAEGTICGHDMCR 607

Db 511 LYDANTQCKWQFGEKAKLCMLDFKKDICKALMCHRIGRKCETKFMPAABGTICGHDMCR 570

QY 608 GGQCVKYGDEGPKPTHGWSWSSWSPCSRTCGGVSHRSLCTNPKPSHGKFCGSTR 667

Db 571 GGQCVKYGDEGPKPTHGWSWSSWSPCSRTCGGVSHRSLCTNPKPSHGKFCGSTR 630

QY 668 TLKLCNSQKCPRDSVDFRAAQCAEHNSRRFRGRHYKWKPYQVEDQDLCKLYCIAEGFDF 727

Db 631 TLKLCNSQKCPRDSVDFRAAQCAEHNSRRFRGRHYKWKPYQVEDQDLCKLYCIAEGFDF 690

QY 728 FFSLSNKKVKGDTPCSEDSRNVCIDGICERVGCDNVLSDAVEDVCGVCGNNSACTIHRG 787

Db 691 FFSLSNKKVKGDTPCSEDSRNVCIDGICERVGCDNVLSDAVEDVCGVCGNNSACTIHRG 750

QY 788 LYTGHHTNQYHHWTTIPSGARSIRIYEMNVSTYSVRNALRRYYLNGHWTVDWFGRYK 847

Db 751 LYTGHHTNQYHHWTTIPSGARSIRIYEMNVSTYSVRNALRRYYLNGHWTVDWFGRYK 810

QY 848 FSGTTFDYRRSYNEPENLIATGPTNETLIVELLFQGRNPGVAMEYSMPRLGTEKQPPAQP 907

Db 811 FSGTTFDYRRSYNEPENLIATGPTNETLIVELLFQGRNPGVAMEYSMPRLGTEKQPPAQP 870

QY 908 SYTWAIVRSECSVSCGGGR 926

Db 871 SYTWAIVRSECSVSCGGGQ 889

RESULT 5

US-10-217-774-4

/ Sequence 4, Application US/10217774

/ Publication No. US20020193583A1

/ GENERAL INFORMATION:

/ APPLICANT: Friddele, Carl Johan

/ APPLICANT: Hilbun, Erin

/ TITLE OF INVENTION: No. US20020193583A1e1 Human Proteases and Polynucleotides Encodin

/ TITLE OF INVENTION: Same

/ FILE REFERENCE: LEX-0219-USA

/ CURRENT APPLICATION NUMBER: US/10/217,774

/ CURRENT FILING DATE: 2002-08-12

/ PRIOR APPLICATION NUMBER: US/09/930,872

/ PRIOR FILING DATE: 2001-08-14

/ PRIOR APPLICATION NUMBER: US 60/225,852

/ PRIOR FILING DATE: 2000-08-16

/ NUMBER OF SEQ ID NOS: 5

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 4

/ LENGTH: 1224

/ TYPE: PRT

/ ORGANISM: homo sapiens

US-10-217-774-4

Query Match 73.5%; Score 3846.5; DB 13; Length 1224;

Best Local Similarity 75.4%; Pred. No. 3.2e-317;

Matches 738; Conservative 25; Mismatches 73; Indels 143; Gaps 13;

QY 1 MKPRARGWGLAALMLLAQVAEQVSPGRSHQGRNGSGQLEASPRLLSRGPRRLTAMS 60

Db 1 MKPRARGWGLAALMLLAQVAEQAP-----ACAMG 31

QY 61 PLPSAGTCVRHGTRSGSAWEPPERPASSSTRGAAGLDGKGRDMDAGNHRSQQTNTGTENO 120

Db 32 PAAAA-----PGSPSVPRPPPPAERPG-----WMKQ----- 58

QY 121 TLHLVLTQYDLVSAEVDHGRGDYVSHHIMHQRRAVAVSEVESLHLRLKGRPHDFHMDL 180

Db 59 -----EYDLVSAEVDHGRGDYVSHHIMHQRRAVAVSEVESLHLRLKGRPHDFHVDL 112

QY 181 RTSSSLVAPGFIVQTLGKTGTSVQTLPPEDFCFYQGSLSHRNSPSHGKFCGSTRTL 240

Db 113 RTSSSLVAPGFIVQTLGKTGTSVQTLPPEDFCFYQGSLSHRNS-SVALSTCGGLSGMI 171

QY 241 KLCNSQKCPRDSVDFRAAQCAEHNSRRFRGR-----HYKWKPYTQVEA-DLCKLYCI 291

Db 172 R-----TEADYFLRLPLPSHLSWKL-GRAQGSPPSHVLYKRSTEPHAPGASEVLVT 222

QY 292 AEGDFEFFS--LSNKKVKGDTPCSEDSRNVCIDGICELSVSTSAHMPQPKEDFILPDE 349

Db 223 SRTWELAHQPLHSDRLRLGP---QKQHF-----GRKKYMPQPKEDFILPDE 270

QY 350 YKSLRHKRSLSLRSHRNEELNVETLVVVDKMMQNNGHENITTYVTLTLNVSALFKD-- 407

Db 271 YKSLRHKRSLSLRSHRNEELNVETLVVVDKMMQNNGHENITTYVTLTLNVSALFKDGT 330

QY 408 -----GLMKDGTTRHDHAILLTGLD 427

Db 331 IGGNINIAIVGLILLEDQPGVLVISHADHTLSSFCQWQSGLMGKDGTTRHDHAILLTGLD 390

QY 428 ICSWKNEPCDTLGFAPISGMSKYSRCTINEDTGLGLAFTIAHESGHPGMTHDGEGNMC 487

Db 391 ICSWKNEPCDTLGFAPISGMSKYSRCTINEDTGLGLAFTIAHESGHPGMTHDGEGNMC 450

QY 488 KXSEGNIMSPITLAGRNGVFSWSPCSRQYLHKFLSTAQAICLADQPKPYKEYKYPKLPGE 547

Db 451 KXSEGNIMSPITLAGRNGVFSWSPCSRQYLHKFLSTAQAICLADQPKPYKEYKYPKLPGE 510

QY 548 LYDANTQCKWQFGEKAKLCMLDFKKDICKALMCHRIGRKCETKFMPAABGTICGHDMCR 607

Db 511 LYDANTQCKWQFGEKAKLCMLDFKKDICKALMCHRIGRKCETKFMPAABGTICGHDMCR 570

QY 608 GGQCVKYGDEGPKPTHGWSWSSWSPCSRTCGGVSHRSLCTNPKPSHGKFCGSTR 667

Db 571 GGQCVKYGDEGPKPTHGWSWSSWSPCSRTCGGVSHRSLCTNPKPSHGKFCGSTR 630

QY 668 TLKLCNSQKCPRDSVDFRAAQCAEHNSRRFRGRHYKWKPYQVEDQDLCKLYCIAEGFDF 727

Db 631 TLKLCNSQKCPRDSVDFRAAQCAEHNSRRFRGRHYKWKPYQVEDQDLCKLYCIAEGFDF 690

QY 728 FFSLSNKKVKGDTPCSEDSRNVCIDGICERVGCDNVLSDAVEDVCGVCGNNSACTIHRG 787

Db 691 FFSLSNKKVKGDTPCSEDSRNVCIDGICERVGCDNVLSDAVEDVCGVCGNNSACTIHRG 750

QY 788 LYTGHHTNQYHHWTTIPSGARSIRIYEMNVSTYSVRNALRRYYLNGHWTVDWFGRYK 847

Db 751 LYTGHHTNQYHHWTTIPSGARSIRIYEMNVSTYSVRNALRRYYLNGHWTVDWFGRYK 810

QY 848 FSGTTFDYRRSYNEPENLIATGPTNETLIVELLFQGRNPGVAMEYSMPRLGTEKQPPAQP 907

Db 811 FSGTTFDYRRSYNEPENLIATGPTNETLIVELLFQGRNPGVAMEYSMPRLGTEKQPPAQP 870

QY 908 SYTWAIVRSECSVSCGGGR 926

Db 871 SYTWAIVRSECSVSCGGGQ 889

RESULT 6

US-10-296-616-2

/ Sequence 2, Application US/10296616

/ Publication No. US20030129658A1

/ GENERAL INFORMATION:

/ APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.

/ TITLE OF INVENTION: No. US20030129658A1e1 protease

/ FILE REFERENCE: Y0132PCT-664

/ CURRENT APPLICATION NUMBER: US/10/296,616

/ PRIOR FILING DATE: 2002-11-26

/ PRIOR APPLICATION NUMBER: JP 2000-393372

/ PRIOR FILING DATE: 2000-12-25

/ NUMBER OF SEQ ID NOS: 26

/ SEQ ID NO 2

/ LENGTH: 1224

/ TYPE: PRT

/ ORGANISM: Homo sapiens

US-10-296-616-2

Query Match 73.5%; Score 3846.5; DB 14; Length 1224;

Best Local Similarity 75.4%; Pred. No. 3.2e-317;

Matches 738; Conservative 25; Mismatches 73; Indels 143; Gaps 13;

QY 1 MKPRARGWGLAALMMLLAQVAEQVSPGRSHQGNRGSGOLEASPPRLLSRGPRLTAMS 60
Db 1 MKPRARGWGLAALMMLLAQVAEQAP-----ACAMG 31
QY 61 PLFSAGTCVRHGTSGSAWEPEPPASSSTRGAAGLDGKGRDMDAAGNHRSQQTNTGTENQ 120
Db 32 PAAAA-----PGSPSVPRPPPPAERPG-----WMEKG----- 58
QY 121 TLHVLTOYDLVSAYEVDHGRGDYVSHEIMHQRRAVAVSEVESLHLRLKGRPHDFHMDL 180
Db 59 -----EYDLVSAYEVDRGDYVSHEIMHQRRAVAVSEVESLHLRLKGSRHDHFVDL 112
QY 181 RTSSSLVAPGFIVQTLGKTGTSVQTLPPEDFCFYQGSLSHRNSPSHGKFCGEGSTRTL 240
Db 113 RTSSSLVAPGFIVQTLGKTGTSVQTLPPEDFCFYQGSLSHRNS-SVALSTCGGLSGMI 171
QY 241 KLCNSQKCPRDSVDFRAAQCAEHNSRRFRGR-----HYKKKPYTOVEA-DLCKLYCI 291
Db 172 R-----TEADYFLRPLPSHLSWKL-GRAAQSSPSHVLTKRSTEPHAPGASEVLVT 222
QY 292 AEGFDFFFS--LSNKVKDGTPCSEDSRNVCIDGICELSVSTSAHMPQPKEDLFILPDE 349
Db 223 SRTWELAHQPLHSSDLRLGLP---QKHFC-----GRRKKYMPQPKEDLFILPDE 270
QY 350 YKSCLRHKRSLRSHRNEELNVETLVVDKKMMQNHGENTTYVLTILNMVSALFKD-- 407
Db 271 YKSCLRHKRSLRSHRNEELNVETLVVDKKMMQNHGENTTYVLTILNMVSALFKDGT 330
QY 408 -----GLMGKDGTRHDHAILLTGLD 427
Db 331 ICGNINIAIVGLILLEDEQPLVISHHADHTLSSFCQWQSGLMGKDGTRHDHAILLTGLD 390
QY 428 ICSWKNEPCDTLGFAPISGMSKYRSCCTINEDTGLGLAFTIAHESGHNFGMIHDGEGNMC 487
Db 391 ICSWKNEPCDTLGFAPISGMSKYRSCCTINEDTGLGLAFTIAHESGHNFGMIHDGEGNMC 450
QY 488 KKSEGNIMSPTLAAGRVFWSWSPCSRQYLHKFLSTAQAICLADQPKPVKEYKYPEKLPG 547
Db 451 KKSEGNIMSPTLAAGRVFWSWSPCSRQYLHKFLSTAQAICLADQPKPVKEYKYPEKLPG 510
QY 548 LYDANTQCKMQFGEKAKLCMLDFKKDICKALMCHRIGRKCETKMPAAEGTICGHDMWCR 607
Db 511 LYDANTQCKMQFGEKAKLCMLDFKKDICKALMCHRIGRKCETKMPAAEGTICGHDMWCR 570
QY 608 GGQCVKYGDEGPKPTHGMSWMSWSPCSRTCGGGVSHRSRLCTNPKPSHGKFCGEGSTR 667
Db 571 GGQCVKYGDEGPKPTHGMSWMSWSPCSRTCGGGVSHRSRLCTNPKPSHGKFCGEGSTR 630
QY 668 TLKLCNSQKCPRDSVDFRAAQCAEHNSRRFRGRHYKKKPYTOVEDQDLCKLYCIAEGFDF 727
Db 631 TLKLCNSQKCPRDSVDFRAAQCAEHNSRRFRGRHYKKKPYTOVEDQDLCKLYCIAEGFDF 690
QY 728 FFSLSNKVKDGTPCSEDSRNVCIDGICERVGCNDVLSDAVEDVCGVCNGNNSACTIHRG 787
Db 691 FFSLSNKVKDGTPCSEDSRNVCIDGICERVGCNDVLSDAVEDVCGVCNGNNSACTIHRG 750
QY 788 LYTKHHTNQYHMTIPSGARSIRIYEMNVSTYSIVRNALRRYYLNGHMTVDMPGRYK 847
Db 751 LYTKHHTNQYHMTIPSGARSIRIYEMNVSTYSIVRNALRRYYLNGHMTVDMPGRYK 810
QY 848 FSGTTFDYRRSYNENPENTATGPTNETLIYELLFOGRNPGVAMEYSMPRLGTEKQPPAQP 907
Db 811 FSGTTFDYRRSYNENPENTATGPTNETLIYELLFOGRNPGVAMEYSMPRLGTEKQPPAQP 870
QY 908 SYTWAIVRSECSVSCGGGR 926
Db 871 SYTWAIVRSECSVSCGGGQ 889

RESULT 7
US-10-804-457-4
; Sequence 4, Application US/10804457

/ Publication No. US20050065334A1
/ GENERAL INFORMATION:
/ APPLICANT: Fridde, Carl Johan
/ APPLICANT: Hilbun, Erin
/ TITLE OF INVENTION: Novel Human Proteases and Polynucleotides Encoding the
/ TITLE OF INVENTION: Same
/ FILE REFERENCE: LEX-0219-USA
/ CURRENT APPLICATION NUMBER: US/10/804,457
/ CURRENT FILING DATE: 2004-03-19
/ PRIOR APPLICATION NUMBER: US/10/217,774
/ PRIOR FILING DATE: 2002-08-12
/ PRIOR APPLICATION NUMBER: US/09/930,872
/ PRIOR FILING DATE: 2001-08-14
/ PRIOR APPLICATION NUMBER: US 60/225,852
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: FastSeq for windows Version 4.0
/ SEQ ID NO 4
/ LENGTH: 1224
/ TYPE: prt
/ ORGANISM: homo sapiens
/ US-10-804-457-4

Query Match 73.5%; Score 3846.5; DB 17; Length 1224;
Best Local Similarity 75.4%; Pred. No. 3.2e-317;
Matches 738; Conservative 25; Mismatches 73; Indels 143; Gaps 13;

QY 1 MKPRARGWGLAALMMLLAQVAEQVSPGRSHQGNRGSGOLEASPPRLLSRGPRLTAMS 60
Db 1 MKPRARGWGLAALMMLLAQVAEQAP-----ACAMG 31
QY 61 PLFSAGTCVRHGTSGSAWEPEPPASSSTRGAAGLDGKGRDMDAAGNHRSQQTNTGTENQ 120
Db 32 PAAAA-----PGSPSVPRPPPPAERPG-----WMEKG----- 58
QY 121 TLHVLTOYDLVSAYEVDHGRGDYVSHEIMHQRRAVAVSEVESLHLRLKGRPHDFHMDL 180
Db 59 -----EYDLVSAYEVDRGDYVSHEIMHQRRAVAVSEVESLHLRLKGSRHDHFVDL 112
QY 181 RTSSSLVAPGFIVQTLGKTGTSVQTLPPEDFCFYQGSLSHRNSPSHGKFCGEGSTRTL 240
Db 113 RTSSSLVAPGFIVQTLGKTGTSVQTLPPEDFCFYQGSLSHRNS-SVALSTCGGLSGMI 171
QY 241 KLCNSQKCPRDSVDFRAAQCAEHNSRRFRGR-----HYKKKPYTOVEA-DLCKLYCI 291
Db 172 R-----TEADYFLRPLPSHLSWKL-GRAAQSSPSHVLTKRSTEPHAPGASEVLVT 222
QY 292 AEGFDFFFS--LSNKVKDGTPCSEDSRNVCIDGICELSVSTSAHMPQPKEDLFILPDE 349
Db 223 SRTWELAHQPLHSSDLRLGLP---QKHFC-----GRRKKYMPQPKEDLFILPDE 270
QY 350 YKSCLRHKRSLRSHRNEELNVETLVVDKKMMQNHGENTTYVLTILNMVSALFKD-- 407
Db 271 YKSCLRHKRSLRSHRNEELNVETLVVDKKMMQNHGENTTYVLTILNMVSALFKDGT 330
QY 408 -----GLMGKDGTRHDHAILLTGLD 427
Db 331 ICGNINIAIVGLILLEDEQPLVISHHADHTLSSFCQWQSGLMGKDGTRHDHAILLTGLD 390
QY 428 ICSWKNEPCDTLGFAPISGMSKYRSCCTINEDTGLGLAFTIAHESGHNFGMIHDGEGNMC 487
Db 391 ICSWKNEPCDTLGFAPISGMSKYRSCCTINEDTGLGLAFTIAHESGHNFGMIHDGEGNMC 450
QY 488 KKSEGNIMSPTLAAGRVFWSWSPCSRQYLHKFLSTAQAICLADQPKPVKEYKYPEKLPG 547
Db 451 KKSEGNIMSPTLAAGRVFWSWSPCSRQYLHKFLSTAQAICLADQPKPVKEYKYPEKLPG 510
QY 548 LYDANTQCKMQFGEKAKLCMLDFKKDICKALMCHRIGRKCETKMPAAEGTICGHDMWCR 607
Db 511 LYDANTQCKMQFGEKAKLCMLDFKKDICKALMCHRIGRKCETKMPAAEGTICGHDMWCR 570
QY 608 GGQCVKYGDEGPKPTHGMSWMSWSPCSRTCGGGVSHRSRLCTNPKPSHGKFCGEGSTR 667

Db 571 GGQCVKYGDEGPKPTHGWSWSSWSPCSRTC GCGGVSHRSRLCTNPKPSHGKFCGSTR 630
Qy 668 TLKLCNSQKCPRDSVDFRAAQCAEHNSRFRGRHYKMKPYTQVEDQDLCKLYCIAEGFDF 727
Db 631 TLKLCNSQKCPRDSVDFRAAQCAEHNSRFRGRHYKMKPYTQVEDQDLCKLYCIAEGFDF 690
Qy 728 FFSLSNKKVKGDTPCSEDSRNVICIDGICERVGCNVLGSDAVEDVCGVCGNNGNSACTIHRG 787
Db 691 FFSLSNKKVKGDTPCSEDSRNVICIDGICERVGCNVLGSDAVEDVCGVCGNNGNSACTIHRG 750
Qy 788 LYTGHHTNQYHMTIPSGARSIRIYEMNVSTSYISVRNALRRYYLNGHMTVDWPGRYK 847
Db 751 LYTGHHTNQYHMTIPSGARSIRIYEMNVSTSYISVRNALRRYYLNGHMTVDWPGRYK 810
Qy 848 FSGTTFDYRRSYNEPENLIATGPTNETLIVELLFQGRNPGVAMEYMPRLGTEKQPPAQP 907
Db 811 FSGTTFDYRRSYNEPENLIATGPTNETLIVELLFQGRNPGVAMEYMPRLGTEKQPPAQP 870
Qy 908 SYTWAIVRSECSVSCGGGR 926
Db 871 SYTWAIVRSECSVSCGGGQ 889

RESULT 8

US-09-981-151A-6

/ Sequence 6, Application US/09981151A

/ Publication No. US20030212256A1

/ GENERAL INFORMATION:

/ APPLICANT: Edinger, Shlomit R

/ APPLICANT: Gerlach, Valerie

/ APPLICANT: MacDougall, John R

/ APPLICANT: Malyankar, Muriel M

/ APPLICANT: Smithson, Glenda

/ APPLICANT: Millet, Isabelle

/ APPLICANT: Peyman, John A

/ APPLICANT: Stone, David J

/ APPLICANT: Gunther, Erik

/ APPLICANT: Ellerman, Karen

/ APPLICANT: Shinkets, Richard A

/ APPLICANT: Padigaru, Muralidhara

/ APPLICANT: Guo, Xiaojia

/ APPLICANT: Paturajan, Meera

/ APPLICANT: Taupier Jr, Raymond J

/ APPLICANT: Burgess, Catherine E

/ APPLICANT: Zernhusen, Bryan D

/ APPLICANT: Kekuda, Ramesh

/ APPLICANT: Spytek, Kimberly A

/ APPLICANT: Gangoli, Beha A

/ APPLICANT: Fernandes, Elma R

/ APPLICANT: Gorman, Linda

/ TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

/ FILE REFERENCE: 21402-168

/ CURRENT APPLICATION NUMBER: US/09/981,151A

/ CURRENT FILING DATE: 2001-10-16

/ PRIOR APPLICATION NUMBER: 60/241,040

/ PRIOR FILING DATE: 2000-10-17

/ PRIOR APPLICATION NUMBER: 60/241,058

/ PRIOR FILING DATE: 2000-10-17

/ PRIOR APPLICATION NUMBER: 60/241,063

/ PRIOR FILING DATE: 2000-10-17

/ PRIOR APPLICATION NUMBER: 60/241,243

/ PRIOR FILING DATE: 2000-10-17

/ PRIOR APPLICATION NUMBER: 60/242,152

/ PRIOR FILING DATE: 2000-10-20

/ PRIOR APPLICATION NUMBER: 60/242,482

/ PRIOR FILING DATE: 2000-10-23

/ PRIOR APPLICATION NUMBER: 60/242,611

/ PRIOR FILING DATE: 2000-10-23

/ PRIOR APPLICATION NUMBER: 60/242,612

/ PRIOR FILING DATE: 2000-10-23

/ PRIOR APPLICATION NUMBER: 60/242,880

/ PRIOR FILING DATE: 2000-10-24

/ PRIOR APPLICATION NUMBER: 60/242,881

/ PRIOR FILING DATE: 2000-10-24
/ Remaining Prior Application data removed - See file wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 160
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 6
/ LENGTH: 856
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-09-981-151A-6

Query Match 64.3%; Score 3365; DB 10; Length 856;
Best Local Similarity 71.9%; Pred. No. 1.5e-276;
Matches 660; Conservative 25; Mismatches 59; Indels 174; Gaps 16;

Qy 129 DLVSAYEVDRGDYVSHIEMHQRRRAVAVSEVESLHLKGRPHDFMDLRTSSSLVA 188
Db 19 DLVSAYEVDRGDYVSHIEMHQRRRAVAVSEVEPAFLQVCRAR---ELRLCVEAFPIA 75
Qy 189 ---PGFI-----VQTIGKTGTSVQTLPPED-----PCFYQ-GSLRS 221
Db 76 NSQPGFLNLSNVSRSHWREQHASKRITITNMILGESALASTRKNVCVFFLSFYFQSGMIRT 135
Qy 222 H-----RNSPSH-----GKFCESG-----TRTLKLCNSQKCPRDSVDFRA 257
Db 136 EADYFLRPLPSHLSWKLGRAAQSSPSHYLYKREVLVTSRTWELAHQ---PLHSSDLRL 192
Qy 258 AQCAEHNSRFRGRHYKMKPYTQVEADLCKLYCIAEGFDFPFSLSNKKVKGDTPCSEDSRN 317
Db 193 GL---PQKHPCGRKK----- 206
Qy 318 VCIDGICELSVSTSAHMPQPKEDFLIPDEYKSCLRHRSLLRSHRNEELNVETLVV 377
Db 207 -----YMPQPKEDFLIPDEYKSCLRHRSLLRSHRNEELNVETLVV 250
Qy 378 DKMMQNHENITTYVTILNMVSALFKD----- 407
Db 251 DKMMQNHENITTYVTILNMVSALFKDGTICGNINIAIVGLILLEDEQGLVISHHA 310
Qy 408 -----GLMGKDGTRHDAILLTGLDICSWKNEPCDTLGFAPISGMSKYRST 455
Db 311 DHTLSSFCQWOSGLMGKDGTRHDAILLTGLDICSWKNEPCDTLGFAPISGMSKYRST 370
Qy 456 INEDTGLAFTIAHESGNFMIHDEGNMCKKSEGNMSPTLAGRNQVSWSPCSRQY 515
Db 371 INEDTGLAFTIAHESGNFMIHDEGNMCKKSEGNMSPTLAGRNQVSWSPCSRQY 430
Qy 516 LHKFLSTAQALCLADQPKPYKEYKYPEKLPGELYDANTQCKWQFGEKAKLMLDFKDDIC 575
Db 431 LHKFLSTAQALCLADQPKPYKEYKYPEKLPGELYDANTQCKWQFGEKAKLMLDFKDDIC 490
Qy 576 KALWCHRIGRKCETKFMPAABGTICGHDMCRGGQCVKYGDEGPKPTHGWSWSSWSPC 635
Db 491 KALWCHRIGRKCETKFMPAABGTICGHEGA-GGQCVKYGDEGPKPTHGWSWSSWSPC 549
Qy 636 SRTCGGVSRSR-LCTNPKPSHGKFCGSTRTLKLCNSQKCPRDSVDFRAAQCAEHNS 694
Db 550 SRTCGGVSRSRQNTHSRPSHGKFCGSTRTLKLCNSQKCPRDSVDFRAAQCAEHNS 609
Qy 695 RFRGRHYKMKPYTQVEDQDLCKLYCIAEGFDFPFSLSNKKVKGDTPCSEDSRNVICIDGIC 754
Db 610 RFRGRHYKMKP-----DQDLCKLYCIAEGFDFPFSLSNKKVKGDTPCSEDSRNVICIDGIC 664
Qy 755 ERVGCNVLGSDAVEDVCGVCGNNGNSACTIHRGLYTKHHTNQYHMTIPSGARSIRIY 814
Db 665 ERVGCNVLGSDAVEDVCGVCGNNGNSACTIHRGLYL-----EYHMTIPSGARSIRIY 718
Qy 815 EMNVSTSYISVRNALRRYYLNGHMTVDWPGRYKFSGTTFDYRRSYNEPENLIATGPTNET 874
Db 719 EMNVSTSYISVRNALRRYYLNGHMTVDWPGRYKFSGTTFDYRRSYNEPENLIATGPTNET 778
Qy 875 LIVELLFQGRNPGVAMEYMPRLGTEKQPPAQPSTYTWAIVRSECSVSCGGGRCLPVLLLE 934
Db 779 LIVELLFQGRNPGVAMEYMPRLGTEKQPPAQPSTYTWAIVRSECSVSCGGGRCLPVLLLE 838

QY 935 AACOPSATAYIALAFLES 952
| | | | |
DB 839 AACOPLATAYIALAFLES 856
| | | | |
RESULT 9
US-10-399-645-4
; Sequence 4, Application US/10399645
; Publication No. US20040029249A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION; LEE, Ernestine A.
; APPLICANT: HAFALIA, April J.A.; YUE, Henry
; APPLICANT: LAL, Preeti G.; YAO, Monique G.
; APPLICANT: LU, Yan; CHAWLA, Nandinder K.
; APPLICANT: WAREEN, Bridget A.; LU, Dyung Aina M.
; APPLICANT: BAUGHN, Mariah R.; DELEGANE, Angelo M.
; APPLICANT: BUREFORD, Neil; BOROWSKY, Mark L.
; APPLICANT: LEE, Sally; XU, Yuming
; APPLICANT: GRIFFIN, Jennifer A.; KALLICK, Deborah A.
; APPLICANT: GANDHI, Ameena R.; ARVIZU, Chandra S.
; APPLICANT: ISON, Craig H.; TANG, Y. Tom
; APPLICANT: AZIMZAI, Yalda; ELLIOTT, Vicki S.
; APPLICANT: SWARNAKAR, Anita; RAMKUMAR, Jayalaxmi
; APPLICANT: NGUYEN, Daniel B.; TRIBOULEY, Catherine M.
; APPLICANT: LO, Terence P.; AU-YOUNG, Janice K.
; APPLICANT: THANGAVELU, Kavitha; KEARNEY, Liam
; TITLE OF INVENTION: PROTEASES
; FILE REFERENCE: PI-0263 USN
; CURRENT APPLICATION NUMBER: US/10/399,645
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: PCT/US01/51034
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: US 60/241,573
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US 60/243,643
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: US 60/245,256
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/248,395
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US 60/249,826
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: US 60/252,303
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,981
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 1236
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040029249A1 3533147CD1
US-10-399-645-4
Query Match 62.8%; Score 3286; DB 15; Length 1236;
Best Local Similarity 93.1%; Pred. No. 1.3e-269;
Matches 591; Conservative 2; Mismatches 0; Indels 42; Gaps 1;
QY 334 HMPQPKEDLFLLPDEYKSCLRHRSILRSHNEBLNVELVVDKMMQNHGHENITTY 393
: | | | | |
DB 268 YMPQPKEDLFLLPDEYKSCLRHRSILRSHNEBLNVELVVDKMMQNHGHENITTY 327
| | | | |
QY 394 VLTILNMSALPKD-----GLMG 411
| | | | |
DB 328 VLTILNMSALPKDGTIGGININIAIVGLILLEDEQPLVISHHADHTLSSFCQWQSGLMG 387
| | | | |
QY 412 KDGRHDHALLLTGLDICSWKNEPCDTLGFAPISGMSKYRSCCTINEDTGLAFTIAHE 471
| | | | |
DB 388 KDGRHDHALLLTGLDICSWKNEPCDTLGFAPISGMSKYRSCCTINEDTGLAFTIAHE 447
| | | | |

QY 472 SGHNFQMTHDGEGNMCKSEGNIMSPTLAGRNVFWSWPCSRQYLHKFLSTAQAICLADQ 531
| | | | |
DB 448 SGHNFQMTHDGEGNMCKSEGNIMSPTLAGRNVFWSWPCSRQYLHKFLSTAQAICLADQ 507
| | | | |
QY 532 PKPVKEYKPEKLPSELVDANTQCKWQGEKAKLCMLDFKKDICKALMCHIRGRKCTKF 591
| | | | |
DB 508 PKPVKEYKPEKLPSELVDANTQCKWQGEKAKLCMLDFKKDICKALMCHIRGRKCTKF 567
| | | | |
QY 592 MPABEGTICGHDMMCRGQCVKYGDEGKPTHGWSWSSWSPCSRCTCGGVSHSRLLCT 651
| | | | |
DB 568 MPABEGTICGHDMMCRGQCVKYGDEGKPTHGWSWSSWSPCSRCTCGGVSHSRLLCT 627
| | | | |
QY 652 NPKPSHGKFCGSTRITLKLNSQKCPRDSVDFRAQCAEHNSRRFRGRHYKMKPYTOVE 711
| | | | |
DB 628 NPKPSHGKFCGSTRITLKLNSQKCPRDSVDFRAQCAEHNSRRFRGRHYKMKPYTOVE 687
| | | | |
QY 712 DQDLCKLYCIAEGFDFPFSLSNKKVKGDTPCSEDSRNVCIDGICERVGCNVLGSDAVEDV 771
| | | | |
DB 688 DQDLCKLYCIAEGFDFPFSLSNKKVKGDTPCSEDSRNVCIDGICERVGCNVLGSDAVEDV 747
| | | | |
QY 772 CGVCGNNSACTIHRGLYTKHHTNQYHMTVTPSGARSIRIYEMNVSTSIYSRNALRR 831
| | | | |
DB 748 CGVCGNNSACTIHRGLYTKHHTNQYHMTVTPSGARSIRIYEMNVSTSIYSRNALRR 807
| | | | |
QY 832 YLLNGHMTVDMPGRYKBSGTFDYRRSYNEPENLIATGPTNETLIVELLFOGRNPGVAME 891
| | | | |
DB 808 YLLNGHMTVDMPGRYKBSGTFDYRRSYNEPENLIATGPTNETLIVELLFOGRNPGVAME 867
| | | | |
QY 892 YSMPLGTEKQPPAQPSYTWAIVRSECSVSCGGGR 926
| | | | |
DB 868 YSMPLGTEKQPPAQPSYTWAIVRSECSVSCGGGR 902
| | | | |
RESULT 10
US-10-240-545A-2
; Sequence 2, Application US/10240545A
; Publication No. US20030185828A1
; GENERAL INFORMATION:
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: No. US20030185828A1el aggreganase
; FILE REFERENCE: 08959.0002
; CURRENT APPLICATION NUMBER: US/10/240,545A
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: PCT/JP01/11033
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: JP 2000-384300
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 2
; LENGTH: 1221
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-240-545A-2
Query Match 46.5%; Score 2435.5; DB 14; Length 1221;
Best Local Similarity 51.3%; Pred. No. 2.7e-197;
Matches 466; Conservative 118; Mismatches 195; Indels 129; Gaps 17;
QY 85 ASSSTRGAAGLDGKGRDMEAGNHRQQTNTGTENQTLHLVLTQYDLVSAEVDHRGDYVS 144
| | | | |
DB 47 ASDSSGASGLN-----DDYVFVTPVEVDSAGSYIS 77
| | | | |
QY 145 HEIMHQRRRAVAASEVESLHLRLKGRHDFHMDLRTSSSLVAPGFIVQTLGKTGTSV 204
| | | | |
DB 78 HDILHNGRKRKS-AQNA RSSLHYRFSAFQGLHLLELK-PSAILSSHPIVQVLGXDGASET 135
| | | | |
QY 205 QTLPPEDFCFYQGSLSHRNSPSHGKFCGSTRITLKLNSQ---KCPRDSVDFRAQC 260
| | | | |
DB 136 QK-PEVOQCIFYQGFIRND-SSSSVAVSTCAGLSGLIRTRKNEFLISPLFQ-----LLA 186
| | | | |
QY 261 AEHNSRRFRGRHYKMKPYTOVEADLCKLYCIAEGFDFPFSLSNKKVXDG-----TPCSBDS 315
| | | | |

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Db 187 QEHNYSSPAG-HHPHVLKYRTAEKIQRYGYPG-----SGRNPYGSPSHI PHASQS 238
QY 316 R-----NVCIDGICELSVSTSAHMPQPKEDLFLPDEYKSLRHKSLRS 363
Db 239 RETEYHHRRLQKHFC-----GRRKKYAPKPTEDTYLRPFDEYSSGGRPRRSAGKS 289
QY 364 HNEBELNVELVVDKMMQNHENITTYVLTILNMVSALFKDG----- 408
Db 290 QKG--LNVELTVVADKKMVEKHGKGNVTYILTVNMVSGLFKDGTTIGSDINVVVSLIL 347
QY 409 -----LMGKDGTRHDHAILLTGLDICSWKNEPCDTLGF 441
Db 348 LEQEPGGLLINHHADQSLNSFCQWQSALIGKNGKRHDHAILLTGFDICSWKNEPCDTLGF 407
QY 442 APISGMSKYSRCTINEDTGLAFTIAHESGHNFGMIHDEGNMCKKSEGNIMSPTLAG 501
Db 408 APISGMSKYSRCTINEDTGLAFTIAHESGHNFGMIHDEGNMCKKSEGNIMSPTLTG 467
QY 502 RNVGFSWSPCSRQYLHKFLSTAQAICLADQPKVKEYKYPEKLPBELYDANTQCKWQFGE 561
Db 468 NNGVFSWSSCSRQYLKKFLSTPQAGCLVDEPKAQGYKYPDKLPQOIYDADTQCKWQFGA 527
QY 562 KAKLCMLDFPKDICKALMCHRIGRKCECTKMPAAEGTICGHDMWCRGGQCVKYGDEGPKP 621
Db 528 KAKLCSLGFVKDICKSLMCHRVGHRCETKMPAAEGTIVCGLSMWCROGQCVKFGELGPRP 587
QY 622 THGHWSWSSWSPCSRTCGGGVSHRSRLCTNPKPSHGKFCBEGSTRTLKLCNSQKCPRDS 681
Db 588 IHGOWSAMSKWSECSRTCGGCVKQERHCNNPKQYQGLFCPSSSRITQLCNINPCNENS 647
QY 682 VDFRAAQCAEHNSRRFRGRHYKWKPYTOVEDQDCLKYCIAEGDFPFSLSNKYKDGTPC 741
Db 648 LDFRAQQCAEYNSKPRFGWFPYQWKPYTKVEEBDRCKLYCKAENFEFFFAMSGKYKDGTPC 707
QY 742 SEDSRNVCIDGICERVGCNDNLGSDAVEDVCGVCNNGNSACTIHRGLYTKHHHTNQYHM 801
Db 708 SPKNKDVCIDGICELVGCDEHLSKAVSDACGVCCKDNSTCKEYKGLYLNQHKANEYYPV 767
QY 802 VTIPSGARSIRIYEMNVSTSYISVNALRRYYLNGHWTVDPGRYKFSGTTFDYRRSYNE 861
Db 768 VIIPAGARSIELOELQVSSSYLAVERLSQKXYLTGWSIDWPGEPFAGTTFEYQRSFNR 827
QY 862 PENLIATGPTNETLIVELLFOGNPVGAVWEYSMPRL--GTEKQPPA--QPSYTWAIVRSE 917
Db 828 PERLYAPGPTNETLIVFEILMQGNPGIAWKYALPKVMNGT--PPATKRPAWTWSIVQSE 884
QY 918 CSVSCGGG 925
Db 885 CSVSCGGG 892
```

```
RESULT 11
US-10-363-937-17
; Sequence 17, Application US/10363937
; Publication No. US20040053269A1
; GENERAL INFORMATION:
; APPLICANT: Todd, Stephen; Delegeane, Angelo M.;
; APPLICANT: Gandhi, Ameena R.; Nguyen, Daniel B.;
; APPLICANT: Hafalia, April J.A.; Kearney, Liam;
; APPLICANT: Lu, Yan; Lee, Ernestine A.;
; APPLICANT: Chawla, Narinder K.; Das, Debopriya;
; APPLICANT: Arvizu, Chandra S.; Yao, Monique G.;
; APPLICANT: Kallick, Deborah A.; Elliott, Vicki S.;
; APPLICANT: Ding, Li; Yue, Henry;
; APPLICANT: Reddy, Roopa; Burford, Neil;
; APPLICANT: Baughn, Mariah R.; Lal, Preeti G.;
; APPLICANT: Borowsky, Mark L.; Lu, Dyung Alna M.;
; APPLICANT: Ramkumar, Jayalaxmi; Yang, Junming;
; APPLICANT: Tribouley, Catherine M.; Khan, Farrah A.;
; APPLICANT: Gururajan, Rajagopal; Tang, Y. Tom;
; APPLICANT: Au-Young, Janice; Warren, Bridget A.;
; APPLICANT: Hernandez, Roberto; Duggan, Brendan M.
; TITLE OF INVENTION: PROTEASES

; FILE REFERENCE: PI-0212 USN
; CURRENT APPLICATION NUMBER: US/10/363,937
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: PCT/US01/28161
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: US 60/231,039
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US 60/232,812
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/234,850
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/236,500
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/238,773
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 60/239,658
; PRIOR FILING DATE: 2000-10-11
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PERL Program
; SEQ ID NO 17
; LENGTH: 1082
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040053269A1 7478405CD1
US-10-363-937-17

Query Match 46.5%; Score 2434.5; DB 15; Length 1082;
Best local Similarity 51.3%; Pred. No. 2.7e-197;
Matches 466; Conservative 118; Mismatches 195; Indels 129; Gaps 17;

QY 85 ASSSTRGAGLDGKGRDMEAGNHSQQTNTGTENQTLHYLTQYDLVSAVEVDHRGDYVS 144
Db 47 ASDSSSGASGLN-----DDYVFVTPEVDSAGSYIS 77
QY 145 HEIMHQRARRA VAVSEVSLHLRLKGRPHDFHMDLRTSSSLVAPGFIVQTLGKTGTSV 204
Db 78 HDILHNGRKRS-AQNAKSSLHYRFSAPGQELHLELK-PSAILSSHFIQVVLGKDGASET 135
QY 205 QTLPPEDFCYQGLSRSHNSPSHGKFCBEGSTRTLKLCNSQ---KCPRDSVDFRAQC 260
Db 136 QK-PEVQQCFYQGFIRND-SSSSVAVSTCAGLSGLIRTRKNEFLISPLPQ-----LLA 186
QY 261 AEHNSRRFRGRHYKWKPYTOVEADCLKYCIAEGDFPFSLSNKYKDG-----TPCSBDS 315
Db 187 QEHNYSSPAG-HHPHVLKYRTAEKIQRYGYPG-----SGRNPYGSPSHI PHASQS 238
QY 316 R-----NVCIDGICELSVSTSAHMPQPKEDLFLPDEYKSLRHKSLRS 363
Db 239 RETEYHHRRLQKHFC-----GRRKKYAPKPTEDTYLRPFDEYSSGGRPRRSAGKS 289
QY 364 HNEBELNVELVVDKMMQNHENITTYVLTILNMVSALFKDG----- 408
Db 290 QKG--LNVELTVVADKKMVEKHGKGNVTYILTVNMVSGLFKDGTTIGSDINVVVSLIL 347
QY 409 -----LMGKDGTRHDHAILLTGLDICSWKNEPCDTLGF 441
Db 348 LEQEPGGLLINHHADQSLNSFCQWQSALIGKNGKRHDHAILLTGFDICSWKNEPCDTLGF 407
QY 442 APISGMSKYSRCTINEDTGLAFTIAHESGHNFGMIHDEGNMCKKSEGNIMSPTLAG 501
Db 408 APISGMSKYSRCTINEDTGLAFTIAHESGHNFGMIHDEGNMCKKSEGNIMSPTLTG 467
QY 502 RNVGFSWSPCSRQYLHKFLSTAQAICLADQPKVKEYKYPEKLPBELYDANTQCKWQFGE 561
Db 468 NNGVFSWSSCSRQYLKKFLSTPQAGCLVDEPKAQGYKYPDKLPQOIYDADTQCKWQFGA 527
QY 562 KAKLCMLDFPKDICKALMCHRIGRKCECTKMPAAEGTICGHDMWCRGGQCVKYGDEGPKP 621
Db 528 KAKLCSLGFVKDICKSLMCHRVGHRCETKMPAAEGTIVCGLSMWCROGQCVKFGELGPRP 587
QY 622 THGHWSWSSWSPCSRTCGGGVSHRSRLCTNPKPSHGKFCBEGSTRTLKLCNSQKCPRDS 681
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Db 588 IHGQWSAWSKWSKSECSRTCCGGVVKFQERHCNNPKRQYGGIFCPGSSRIYQLCNINPCNENS 647
QY 682 VDFRAAQCAEHNRRFRGRHYKWKPYTQVEDQDLCKLYCIAEGFDFEFSLSNKVKDGTPC 741
Db 648 LDFRAOQCAEYNSKPRFGWFYQWKPYTKVEEEDRCKLYCKAENFEFFFAMSGVKDGTPC 707
QY 742 SEDSRNVCIDGICERVGCNDVLSDAVEDVCGVCGNNGNSACTIHRGLYTKHHHTNQYYHM 801
Db 708 SPKNNDVICIDGVCGLVGCDELGSKAVSDACGVCKGDNSTCKEYKGLYLNGHKANEYYPV 767
QY 802 VTIPSGARSIRIYEMNVSTYSVRNALRRYYLNGHWTVDWPGRYKFSGTTPDYRRSYNE 861
Db 768 VIPAGARSIEIQELQVSSSYLAVRSLSQKYYLTGWSIDWPGEFEPFAGTTFEYQRSFNR 827
QY 862 PENLIATGPTNETLIVELLFOGRNPGVAMEYSMPRL--GTEKOPPA--QPSYTWAIVRSE 917
Db 828 PERLYAPGPTNETLVFEILMQGNPGIAWKYALPKVMNGT---PPATKRPAWTWSIVQSE 884
QY 918 CSVSCGGG 925
Db 885 CSVSCGGG 892

RESULT 12
US-10-354-983-2
; Sequence 2, Application US/10354983
; Publication No. US20040044194A1
; GENERAL INFORMATION:
; APPLICANT: AGOSTINO, MICHAEL J.
; APPLICANT: CORCORAN, CHRISTOPHER
; TITLE OF INVENTION: AGGREGANASE MOLECULES
; FILE REFERENCE: 08702.0111-00000
; CURRENT APPLICATION NUMBER: US/10/354,983
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: 60/353,680
; PRIOR FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-354-983-2

Query Match 46.5%; Score 2434.5; DB 15; Length 1221;
Best Local Similarity 51.3%; Pred. No. 3.3e-197;
Matches 466; Conservative 118; Mismatches 195; Indels 129; Gaps 17;
QY 85 ASSSTRGAAGLDGKGRDMEAGNHRSQQTNTGTENTLHVLTOYDLVSAVEVDHRGDYVS 144
Db 47 ASDSSSGASGLN-----DDYVFTVPEYVDSAGSYIS 77
QY 145 HEIMHQRRAVAVSEVESLHLRLKGRPHDPMDLRTSSSLVAPGFIVQTLGKTGTSKV 204
Db 78 HDILHNGRKKRS-AQNAARSSLHYRFSAFQGLHLLELK-PSAILSSHFIYQVLGKDGASET 135
QY 205 QTLRPEDFCFYQGSLSHRNPSHGKFCBEGSTRTLKLCNSQ---KCPRDSVDFRAQC 260
Db 136 QK-PEVQOCFYQGFIRND-SSSSVAVSTCAGLSGLIRTRKNEFLISPLPQ-----LLA 186
QY 261 AEHNSRRFRGRHYKWKPYTQVEADLCKLYCIAEGFDFEFSLSNKVKDG-----TPCSEDS 315
Db 187 QEHNHSSPAG-HHPHVLKYRTAEKIQRYYRGP-----SGRNPYGPSPSHI PHASQS 238
QY 316 R-----NVCIDGICELSVSTSAHMPQPKEDLFILPDEYKSLRHKRSLRS 363
Db 239 RETEYHHRRLQKHFC-----GRRKKYAPKPTEDTYLRPDEYGSSEGRPRRSAGKS 289
QY 364 HRNBLNVEITLVVVDKQMONGHENITTYVLTILNVSALFEKD----- 408
Db 290 QKG--LNVEITLVVADKQWBEKGKGNVTYILITVMNVSGLFKDGITGSDINVVVSLIL 347

QY 409 -----LMGKDGRHDHAILLTGLDICSWKNEPCDTLGF 441
Db 348 LEQEPGGLLINHHADQSLNSFCQWQSAIIGKNGKRHDHAILLTGFDICSWKNBPCDTLGF 407
QY 442 APISGCKYRSCTINEDTGLGLAFTTAHESGHNFGMIHDEGNMCKKSEGNIMSPTLAG 501
Db 408 APISGCKYRSCTINEDTGLGLAFTTAHESGHNFGMIHDEGNPCRKAGNIMSPTLTG 467
QY 502 RNVFWSWPCSRQYLHKFLSTAQALCLADQPKPVKEYRPEKLPGELYDANTQCKWQFGE 561
Db 468 NNGVFSWSSCSRQYLKKFLSTPQAGCLVDEPKQAGQYKYPDKLPQIYDADTQCKWQFGA 527
QY 562 KAKLCMLDFKKDICKALMCHIRIGRKCTKFMPAABGTICGHDMMCRGQCVKYGDEGPKP 621
Db 528 KAKLCSLGFVKDICKSLMCHRVGHRCEYKFMPAABGTICGLSMWCRQGCVKFGELGPRP 587
QY 622 THGWSWSSWSPCSRTCGGGVSHRSRLCTNPKPSHGKFCBEGSTRTLKLCNSQKCPRDS 681
Db 588 IHGQWSAWSKWSKSECSRTCCGGVVKFQERHCNNPKRQYGGIFCPGSSRIYQLCNINPCNENS 647
QY 682 VDFRAAQCAEHNRRFRGRHYKWKPYTQVEDQDLCKLYCIAEGFDFEFSLSNKVKDGTPC 741
Db 648 LDFRAOQCAEYNSKPRFGWFYQWKPYTKVEEEDRCKLYCKAENFEFFFAMSGVKDGTPC 707
QY 742 SEDSRNVCIDGICERVGCNDVLSDAVEDVCGVCGNNGNSACTIHRGLYTKHHHTNQYYHM 801
Db 708 SPKNNDVICIDGVCGLVGCDELGSKAVSDACGVCKGDNSTCKEYKGLYLNGHKANEYYPV 767
QY 802 VTIPSGARSIRIYEMNVSTYSVRNALRRYYLNGHWTVDWPGRYKFSGTTPDYRRSYNE 861
Db 768 VIPAGARSIEIQELQVSSSYLAVRSLSQKYYLTGWSIDWPGEFEPFAGTTFEYQRSFNR 827
QY 862 PENLIATGPTNETLIVELLFOGRNPGVAMEYSMPRL--GTEKOPPA--QPSYTWAIVRSE 917
Db 828 PERLYAPGPTNETLVFEILMQGNPGIAWKYALPKVMNGT---PPATKRPAWTWSIVQSE 884
QY 918 CSVSCGGG 925
Db 885 CSVSCGGG 892

RESULT 13
US-10-120-801-48
; Sequence 48, Application US/10120801
; Publication No. US20030203843A1
; GENERAL INFORMATION:
; APPLICANT: Pena, Carol
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shimkets, Richard
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly
; APPLICANT: Mehraban, Fuad
; APPLICANT: Topper, James N.
; APPLICANT: Malyankar, Uriel
; APPLICANT: Wasserman, Scott
; APPLICANT: Edinger, Shlomit
; APPLICANT: Smithson, Glenda
; APPLICANT: Gunther, Erik
; APPLICANT: Komuves, Laszlo
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-340
; CURRENT APPLICATION NUMBER: US/10/120,801
; PRIOR APPLICATION NUMBER: 60/285748
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 60/286068
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/286292
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/288334
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 60/291241

; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 60/322284
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/285609
; PRIOR FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 1365
; TYPE: PRT
; ORGANISM: human
US-10-120-801-48

Query Match 46.4%; Score 2430; DB 15; Length 1365;
Best Local Similarity 61.5%; Pred. No. 9.3e-197;
Matches 479; Conservative 10; Mismatches 30; Indels 260; Gaps 10;

QY 335 MQQPPKEDLFLPDEYKSCLRHKSLLRSHRNEINVELLVVDKMMQNHENITTYV 394
DB 1 MQQPPKEDLFLPDEYKSCLRHKSLLRSHRNEINVELLVVDKMMQNHENITTYV 60
QY 395 LTIINMVSALFKD-----GLMGK 412
DB 61 LTIINMVSALFKDGTIGNNINAIIVGLILLEDEQGLVISHHADTLSSFCQWQSGLMGK 120
QY 413 DGRHDHAILLTGLDICSWKNEPCDTLGFAPISGMSKYRSCCTINEDTGLAFTIAHES 472
DB 121 DGRHDHAILLTGLDICSWKNEPCDTLGFAPISGMSKYRSCCTINEDTGLAFTIAHES 180
QY 473 GH-----NFGMIHDG-----EGNM-----CKK 489
DB 181 GHKGDYVEYSANYEWSRGMSDAGREQATVPRNCCQLQLSLSFMEGELCFSRCLHEACVR 240
QY 490 SEGNIMSPTLA-----GRNGVFS-----WSPCSRQYLHKFLSTAQAICL 528
DB 241 ALGSSVLPLVVAIIMPCKQGDGSKTRGQALSCGGEKDRGNQFMSCSRMSGKVFGGTAQAICL 300
QY 529 ADQPKPVKEYKYPEKLPGLLYDANTQCKWQFGEKAKLCMLDPFK----- 572
DB 301 ADQPKPVKEYKYPEKLPGLLYDANTQCKWQFGEKAKLCMLDPFKASMAHQPPAAGLYAP 360
QY 573 -----DICKALMCHRIGRKCETKFMPAEGTI 599
DB 361 SVQEASVSRPGAOSLSLVSRSDLSYCHPDIIBPDICKALMCHRIGRKCETKFMPAEGTI 420
QY 600 CGHDMWCRGGQCVKYKDEGPKPTHGHWSDWSSWSPCSRTCGGVSHRSLCTNPKPSHGG 659
DB 421 CGHDMWCRGGQCVKYKDEGPKPTHGHWSDWSSWSPCSRTCGGVSHRSLCTNPKPSHGG 480
QY 660 KFCGEGSTRTLKLCNSQKCPRDSVDFRAQAQCAEHNSRRFRGRHYKMKPYTOVEDODLCKLY 719
DB 481 KFCGEGSTRTLKLCNSQKCPRDSVDFRAQAQCAEHNSRRFRGRHYKMKPYTOVE----- 532
QY 720 CIAEGFDFPFSLSNKVKDGTPCSSEDSRNVCIDGICERVGCDNVLGSDAVEDVCGVCGNGNN 779
DB 533 ----- 532
QY 780 SACTIHRGLYTKHHHTNOYYHMTIPSGARSIRIYEMNVSTSYISVRNALRRYYLNGHWT 839
DB 533 -----EYHMTIIPSGARSIRIYEMNVSTSYISVRNALRRYYLNGHWT 575
QY 840 VDMFGRYKFSGTTFDYRRSYNEPENLIATGPTNETLIVELLFQGRNPGVAMEYSMPRLGT 899
DB 576 VDMFGRYKFSGTTFDYRRSYNEPENLIATGPTNETLIVELLFQGRNPGVAMEYSMPRLGT 635
QY 900 EKQPPAQPSYTWAIVRSECSVSCGG-----RCL-----PVLLEAACQ 938
DB 636 EKQPPAQPSYTWAIVRSECSVSCGGGLNVCKFGALKMGDYCLYPDGLHFPPLPLTISQGCQ 694

RESULT 14
US-10-354-983-4
; Sequence 4, Application US/10354983

; Publication No. US20040044194A1
; GENERAL INFORMATION:
; APPLICANT: AGOSTINO, MICHAEL J.
; APPLICANT: CORCORAN, CHRISTOPHER
; TITLE OF INVENTION: AGGREGANASE MOLECULES
; FILE REFERENCE: 08702.0111-00000
; CURRENT APPLICATION NUMBER: US/10/354,983
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: 60/353,680
; PRIOR FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1071
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-354-983-4

Query Match 46.1%; Score 2411.5; DB 15; Length 1071;
Best Local Similarity 51.3%; Pred. No. 2.4e-195;
Matches 466; Conservative 117; Mismatches 194; Indels 131; Gaps 19;

QY 85 ASSSTRGAAGLDGKGRDMEAGNHRSQQTNTGTENOTLHVLTQYDLVSAEYVDHGRDYVS 144
DB 24 ASDSSSGASGLN-----DDYVFTVPVEVDSAGSYIS 54
QY 145 HEIMHQRRAVAVSEVESLHLRLKGRPHDFMDLRTSSSLVAPGFIYQTLGKTGTSV 204
DB 55 HDILHNGRKGRS-AQNAASSLHYRFSAFQGLHLELK-PSAILSSHFIQVQLKDGASET 112
QY 205 QTLPPEDFCFYQGLSRSHRNSPSHGGKFCGEGSTRTLKLCNSQ---KCPRDSVDFRAQC 260
DB 113 QK-PEVQOCFYQGFIRND-SSSSVAVSTCAGLSGLIRTRKNEFLISPLPQ-----LLA 163
QY 261 AEHNSRRFRGRHYKMKPYTOVEADLCKLYCIAEGDFPFSLSNKVKDG-----TPCSEDS 315
DB 164 QEHNSSPAG-HHPVLVYKRTABEKLQRYRGYPG-----SGRNPFGYSFSHIIPHASQS 215
QY 316 R-----NVCIDIGCELSVSTSAAMPQPPKEDLFLPDEYKSCLRHKSLLRS 363
DB 216 RETEYHHRRLQKQHC-----GRRKYAPKPPTEDTYLRFDEYSSGRPRRSAGKS 266
QY 364 HRNEBLNVELLVVDKMMQNHENITTYVLTILNMVSALFKD----- 408
DB 267 QKG-LNVELLVADKQVKEHKGKGNVTYTLTVMNMVSGLFKDGITGSDINVVVSLIL 324
QY 409 -----LMKDGTRHDHAILLTGLDICSWKNEPCDTLGF 441
DB 325 LEQEPGLLINHHADQSLNSFCQWQSALIGKNGKRHDHAILLTGLDICSWKNEPCDTLGF 384
QY 442 APISGMSKYRSCCTINEDTGLAFTIAHESGHNFGMIHDEGNMCKSEGNIMSPTLAG 501
DB 385 APISGMSKYRSCCTINEDTGLAFTIAHESGHNFGMIHDEGNMCKSEGNIMSPTLTG 444
QY 502 RNVFSPWSPCSRQYLHKFLSTAQAICLADQPKPVKEYKYPEKLPGLLYDANTQCKWQFGE 561
DB 445 NNGVFSWSSCSRQYLKKFLSTPQAAGCLVDEPKQAQGYKYPDKLPGLIYDADTQCKWQFGA 504
QY 562 KAKLCMLDPFKDKICKALMCHRIGRKCETKFMPAEGTICGHDWCRGGQCVKYKDEGPKP 621
DB 505 KAKLCSLGFVNDICKSLWCHRVGHRCECTKEMPAEGTVCGLSMWCRQGQCVYFG-LGPRP 563
QY 622 THGHWSDWSSWSPCSRTCGGGVSHRSRLCTNPKPSHGGKFCGEGSTRTLKLCNSQKCPRDS 681
DB 564 IHQWSAWSKWSSECSRTCGGKVFQERHCHNNPKPQYGGIIFCGSSRIYQLCNINPCNENS 623
QY 682 VDFRAQAQCAEHNSRRFRGRHYKMKPYTOVEDODLCKLYCIAEGDFPFSLSNKVKDGTPC 741
DB 624 LDFRAQAQCAEYNSKPFGRGWFYQWKPYTKVEEDRCKLYCKAENFEFFPAMSGKVKDGTPC 683
QY 742 SEDSRNVCIDGICERVGCDNVLGSDAVEDVCGVCGNGNSACTIHRGLYTKHHHTNOYYHM 801
DB 684 SPNRNDVICIDGCELVGCDHEIGSKAVSDACGVC-GDNSTCKFYKGLYLNGHKANEYYPV 742

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 9, 2005, 22:16:24 ; Search time 375 Seconds
(without alignments)
4153.961 Million cell updates/sec

Title: US-09-981-151D-8
Perfect score: 5236
Sequence: 1 MKPRARGWRLAALWMLAQ.....LEAACQPSATAYIALAFLES 952

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=Issued Patents NA -QFMT=fastap -SUFFIX=rn1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pcr -THR MAX=100 -THR MIN=0 -ALIGN=15
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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- 5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3981.5	76.0	3675	3	US-09-930-872-3 Sequence 3, Appl1
2	3981.5	76.0	3675	4	US-10-217-774-3 Sequence 3, Appl1
3	3981.5	76.0	4042	3	US-09-930-872-5 Sequence 5, Appl1
4	3981.5	76.0	4042	4	US-10-217-774-5 Sequence 5, Appl1
5	1678.5	32.1	1476	3	US-09-930-872-1 Sequence 1, Appl1
6	1678.5	32.1	1476	4	US-10-217-774-1 Sequence 1, Appl1
7	1390	26.5	2272	4	US-09-963-791-1 Sequence 1, Appl1
8	1319	25.2	2274	4	US-09-963-791-23 Sequence 23, Appl1
9	1284	24.5	3160	4	US-09-963-791-25 Sequence 25, Appl1
10	1247.5	23.8	3571	4	US-09-799-451-411 Sequence 411, App
11	1245.5	23.8	5357	3	US-09-392-184-5 Sequence 5, Appl1
12	1243	23.7	3377	4	US-09-981-953A-3 Sequence 3, Appl1

13	1237	23.6	3766	4	US-09-981-953A-1 Sequence 1, Appl1
14	1218	23.3	2848	3	US-09-369-364A-4 Sequence 4, Appl1
15	1186	22.7	3218	3	US-09-369-364A-6 Sequence 6, Appl1
16	1102.5	21.1	3885	3	US-09-369-364A-16 Sequence 16, Appl1
17	1056	20.2	5804	3	US-09-369-364A-12 Sequence 12, Appl1
18	1010	19.3	4676	3	US-09-130-491-1 Sequence 1, Appl1
19	997.5	19.1	3889	4	US-09-568-559-1 Sequence 1, Appl1
20	997	19.0	4858	3	US-09-392-184-1 Sequence 1, Appl1
21	991	18.9	2625	3	US-09-369-364A-14 Sequence 14, Appl1
22	969	18.5	6659	4	US-09-321-987B-1 Sequence 1, Appl1
23	961.5	18.4	4580	3	US-09-491-522-8 Sequence 8, Appl1
24	958.5	18.3	2184	4	US-09-445-023A-13 Sequence 13, Appl1
25	949	18.1	3636	4	US-09-949-016-5530 Sequence 5530, Ap
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27	934	17.8	2184	4	US-09-445-023A-2 Sequence 2, Appl1
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29	920.5	17.6	3706	3	US-09-484-970B-58 Sequence 58, Appl
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32	885.5	16.9	3002	3	US-09-369-364A-1 Sequence 1, Appl1
33	878	16.8	3250	3	US-09-122-126B-14 Sequence 14, Appl
34	878	16.8	3250	4	US-09-634-286A-14 Sequence 14, Appl
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36	856.5	16.4	4192	3	US-09-122-126B-1 Sequence 1, Appl1
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39	839.5	16.0	3638	3	US-09-369-364A-8 Sequence 8, Appl1
40	776.5	14.8	1770	4	US-09-963-791-11 Sequence 11, Appl1
41	755.5	14.4	3126	3	US-09-392-184-7 Sequence 7, Appl1
42	705.5	13.5	1317	4	US-09-963-791-21 Sequence 21, Appl1
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44	578.5	11.0	1524	4	US-09-963-791-9 Sequence 9, Appl1
45	550	10.5	3158	4	US-09-949-016-1988 Sequence 1988, Ap

ALIGNMENTS

RESULT 1
US-09-930-872-3
; Sequence 3, Application US/09930872
; Patent No. 6448388
; GENERAL INFORMATION:
; APPLICANT: Fridde, Carl Johan
; APPLICANT: Hilbun, Erin
; TITLE OF INVENTION: No. 6448388e1 Human Proteases and Polynucleotides Encoding the San
; FILE REFERENCE: LEX-0219-USA
; CURRENT APPLICATION NUMBER: US/09/930,872
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,852
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3675
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-930-872-3

Alignment Scores:

Pred. No.: 0
Score: 3981.50
Length: 3675
Matches: 764
Percent Similarity: 78.26%
Best Local Similarity: 76.55%
Conservative: 17
Query Match: 76.04%
Mismatch: 38
Indels: 181
Gaps: 10
DB: 3

US-09-981-151D-8 (1-952) x US-09-930-872-3 (1-3675)

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QY 21 ValAlaGlnValSerProGlyArgSerHisGlnArgGlyAsnArgGlySerGlyGln 40

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QY      81 ProGluArgProAlaSerSerSerThrArgGlyAlaAlaGlyLeuAspGly-LysGlyArg 100
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QY      100 GasPmetAspGluAlaGlyAsnHisArgSerGlnGlnThrAsnThrGlyThrGluAsnGly 120
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QY      120 nThrLeuHisValLeuThrGlnTyrAspLeuValSerAlaTyrGluValAspHisArgGly 140
Db      175 -----GAATATGACCTGGTCTCTGCTTACGAGGTTCACACAGGGG 215
QY      140 yAspTyrValSerHisGlyIleMetHisHisGlnArgArgArgAlaValAlaValSe 160
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QY      160 rGluValGlySerLeuHisLeuArgLeuLysGlyProArgHisAspPheHisMetAspLe 180
Db      276 CGAGGTGAGTCTCTTCACTTCGGCTGAAAGGCTCCAGGCGACGACTTCACGCTGATCT 335
QY      180 uArgThrSerSerSerLeuValAlaProGlyPheIleValGlnThrLeuGlyLysThrGly 200
Db      336 GAGGACTTCAGCAGCCCTAGTGGCTCTGGCTTTATTGTGCAGACGTTGGGAAAGACAGG 395
QY      200 yThrLysSerValGlnThrLeuProProGluAspPheCysPheTyrGlnGlySerLeuArg 220
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Db      456 ATCACACAGAAACTCC--TCAGTGGCCCTTCAACCTGCCAAGGCTTGTCAAGGCATGAT 512
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QY      320 leAspGlyTyrLeuSerGluLeuSerValValSerThrSer-----AlaHis----- 334
Db      639 TCCTT-GGGGCCAGTGAAGTCTGTGGTGAAGCTCAAGACATGGAGCTGGCATCAACCCC 697
QY      334 ----- 334
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QY      335 -----MetProGlnProProLysGluAspLeuPheIleLeuProAspGluTyrLys 352
Db      758 AGAATAATACATGCCCCAGCGCTCCCAAGGAAGACCTTTCATCTTGCCAGATGATATAAGT 817
QY      352 erCysLeuArgHisLysArgSerLeuLeuArgSerHisArgAsnGlnGluLeuAsnValG 372
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Db      878 AGACCTTGGTGTGTGCACAAAGAAATGATGCAAAACCATATGCCATGAAATATCACCA 937
QY      392 hrTyrValLeuThrIleLeuAsnMetValSerAlaLeuPheLysAsp----- 407
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QY      408 -----GlyLeuM 410
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QY      430 erTyrLysAsnGluProCysAspThrLeuGlyPheAlaProIleSerGlyMetCysSerL 450
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QY      450 yTyrArgSerCysThrIleAsnGluAspThrGlyLeuGlyLeuAlaPheThrIleAlaH 470
Db      1238 AATATCGACGTGCACACATTAATGAAGATACAGGCTTGGAAGTGGCTTCAACATTTGCC 1297
QY      470 iSgIuSerGlyHisAsnPheGlyMetIleHisAspGlyGlnGlyAsnMetCysLysLys 490
Db      1298 ATGAGTGTGACACACAACCTTTGGCATGATTCATGATGAGGAAGGAACAATGTAAGT 1357
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QY      590 ySPheMetProAlaAlaGlnGlyThrIleCysGlyHisAspMetTrpCysArgGlyGlyG 610
Db      1658 AATTATGCCAGCAGCAGAGCAACAATTTGTGGCATGACATGTGTGCCGGGAGGAGC 1717
QY      610 InCysValLysTyrGlyAspGlnGlyProLysProThrHisGlyHisTyrPheAspTrp 630
Db      1718 AGTGTGGAATATATGTGATGAAGGCCCAAGCCCAAGCCCATGCGCATGCTGGACTGGT 1777
QY      630 erSerTrpSerProCysSerArgThrCysGlyGlyValSerHisArgSerArgLeu 650
Db      1778 CTTCCTGGTCCCATGCTCCAGGACTGCGGAGGGAGATATCTCATAGAGAGTCCGCTCT 1837
QY      650 ySThrAsnProLysProSerHisGlyGlyLysPheCysGlnGlySerThrArgThrLeu 670
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QY      670 yLeuCysAsnSerGlnLysCysProArgAspSerValAspPheArgAlaAlaGlnCysA 690
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DB	2018	TAGAAGATCAGGACTTATGCAAACTCTACTGTATCGCAAGAGGATTGATTTCTTTT	2077
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QY	750	leASrGLYlLeCYsGLWArGVAlGLCYsASrASnVAlLeuGLYSerASrAlaVAlGLW	770
DB	2138	TAGATGGGATATGTGAGAGAGTTGGATGTGCAATGTCTTGATCTGATGTGTGAAG	2197
QY	770	sPVALCYsGLYVAlCYsASnGLYASnASnSerAlaCYsThrILeHISArGLYLeuTYrT	790
DB	2198	ACGTCTGTGGGTGTGTAAcGGGAATACTCAcCTGCACGATTCACAGGGGTCTTACA	2257
QY	790	hrlYsHIShISrThrASnGLINTYrThrHISmetVAlThrILeProSerGLYAlAArgS	810
DB	2258	CCAAGCACCAcCACCAcCAcGATATTATCAcATGTCAcCATTCCTTCTGAAGCCCGA	2317
QY	810	erILeArGLleTYrGLWmetASnVAlSerThrSerTYrILeSerVAlArGASnAlAleuA	830
DB	2318	GTATCCGCATCTATGAATGAACGTCTCTACTCTCATATTCTGTGCGCATGCCCTCA	2377
QY	830	rgArGLTYrTYrLeuASnGLYHISrThrVAlASrTrPProGLYArGLYrLYsPheSerG	850
DB	2378	GAAgGTACTACTGAATGGGCACTGGACCGTGACTGGCCGGCCGGTACAATTTTCGG	2437
QY	850	LYThrThrPheASrTYrARgArGSerTYrASnGLUProGLWASnLeuILeAlaThrGLYp	870
DB	2438	GCACTACTTTGCACTACAGACGGTCTTATATGAACCCGAGAACTTAATCGTACTGAC	2497
QY	870	roThrASnGLUThrLeuILeVAlGLULeuLeuPheGLNGLYARgASnProGLYVAlAlAT	890
DB	2498	CAACCAACGAGACACTGATTGTGAGCTGCTGTTCAGGGAAGAAACCCGGGTGTGGCT	2557
QY	890	rPGLTYrSermetProArGLeUGLYThrGLYsGLNProProAlaGLNProSerTYrT	910
DB	2558	GGGAATACTCATGCTCGCTTGGGGACCGAAGACGCCCTCGCCACGCCACGTACA	2617
QY	910	hrrTrPAlaILeVAlArGserGLUCYsSerVAlSerCYsGLYGLYGLYArg	926
DB	2618	CTTGGGCATCGTCGCTCTGAGTGTCTCGGTCTCTGCGGAGGGGAGAC	2667

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RESULT 2
US-10-217-774-3
; Sequence 3, Application US/10217774
; Patent No. 6734007
; GENERAL INFORMATION:
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Hilbun, Erin
; TITLE OF INVENTION: No. 6734007e1 Human Proteases and Polynucleotides Encoding the
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0219-USA
; CURRENT APPLICATION NUMBER: US/10/217,774
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US/09/930,872
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,852
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3675
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-217-774-3

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Alignment Scores:		
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Percent Similarity:	78.26%	Conservative: 17
Best Local Similarity:	76.55%	Mismatches: 38
Query Match:	76.04%	Indels: 181
DB:	4	Gaps: 10

US-09-981-151D-8 (1-952) x US-10-217-774-3 (1-3675)

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QY	21	ValAlaGluGlnValSerProGlyArgSerHisGlnArgGlyAsnArgGlySerGlyGln	40
Db	61	GTGGCCGAGCA-----	71
QY	41	LeuGluAlaSerProProArgLeuLeuSerArgGlyProArgArgLeuThrAlaMetSer	60
Db	71	-----	71
QY	61	ProLeuPheSerAlaGlyThrCysValArgHisGlyThrArgSerGlySerAlaTrpGlu	80
Db	72	-----GGCACCTGCGTGGCCATGGGACCCGCAAGCGGCAAGCGCTGGGAG	116
QY	81	ProGluArgProAlaSerSerSerThrArgGlyAlaAlaGlyLeuAspGly-LysGlyArg	100
Db	117	CCCGAGCGTCCCGCGTCTCTCCACCCGCGGAGCGCGCGGCTGGATGGAAAAAGGCG--	174
QY	100	GAspMetAspGluAlaGlyAsnHisArgSerGlnGlnThrAsnThrGlyThrGluAsnGly	120
Db	174	-----	174
QY	120	nThrLeuHisValLeuThrGlnTyrAspLeuValSerAlaTyrGluValAspHisArgGly	140
Db	175	-----GAATATGAACTGGTCTCTGCTACGAGTTGACCAACACAGGGG	215
QY	140	YAspTyrValSerHisGluIleMetHisHisGlnArgArgArgArgAlaValAlaValSer	160
Db	216	CGATTACGTGTCCCATGAATCATGCACCATCAGCGGCGGAGAAGACAGTGGCCGTGTC	275
QY	160	rgluValGluSerLeuHisLeuArgLeuLysGlyProArgHisAspPheHisMetAspLeu	180
Db	276	CGAGGTGAGTCTTCACTTGCGCTGAAGGCTCCAGGACGACTTCCACGTGATCT	335
QY	180	uArgThrSerSerSerLeuValAlaProGlyPheIleValGlnThrLeuGlyLysThrGly	200
Db	336	GAGGACTTCCAGCAGCCTAGTGGCTCTGGCTTATTTGTGCAGACGTTGGGAAAGACAGG	395
QY	200	YThrLysSerValGlnThrLeuProProGluAspPheCysPheTyrGlnGlySerLeuArg	220
Db	396	CACATAAGTCTGTGCAGACTTATCCGCCAGAGACTTCTGTTCTATCAAGGCTCTTTGCG	455
QY	220	gSerHisArgAsnSerProSerHisGlyGlyLysPheCysGluGlySerThrArgThrLeu	240
Db	456	ATCACACAGAACTCC--TCAATGGCCCTTTCAACTGCCAAGGCTTGTCAAGCATGAT	512
QY	240	uLysLeuCysAsnSerGlnLysCysProArgAspSerValAspPheArgAlaAlaGlnCys	260
Db	513	ACGA-----ACAGAAGAGGACAGATTACTTCTTAAGGCCACT	548
QY	260	sAlaGluHisAsnSerArgArgPheArgGlyArgHisTyrLysTyrLysProTyrThrGly	280
Db	549	TCCTTCACACACTCTCA-----TGAAAA-----	570
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Db	571	-----CTCGGACAGAG-----	580
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QY	320	leaspGlyIleCysGluLeuSerValSerThrSer-----AlaHis-----	334
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QY	334	-----	334
Db	698	TGCACAGCAGCGACCTTCGCTGGGACTGCCACAAAGCAGCATTTCTGTGAAGACGCA	757
QY	335	-----MetProGlnProProLySGluAspLeuPheIleuProAspGluTyrLys	352
Db	758	AGAAATACATGCCCCAGCCTCCCAAGGAGACCTTCATCTTGGCCAGATGATATAAGT	817
QY	352	erCysLeuArgHisLysArgSerIleuLeuArgSerHisArgAsnGluGluLeuAsnValG	372
Db	818	CTTGCTTACGGCATTAAGCGCTCTCTTCTGTAGGTCCTCATAGAAATGAAGAACTGAACGTGG	877
QY	372	IuThrLeuValValAlaAspLysLysMetMetGlnAsnHisGlyHisGluAsnIleThrT	392
Db	878	AGACCTTGGTGGTGGTCGACAAAAGATGATGCAAAACCATGGCCATGAATAATCACCA	937
QY	392	hTyrValLeuThrIleLeuAsnMetValSerAlaLeuPheLysAsp-----	407
Db	938	CCTACGTGCTCAGCATACTCAACATGGTATCTGCTTATTCAAGAATGGAACAATAGAG	997
QY	407	-----	407
Db	998	GAACATCAACATTGCATTTGAGTCTGATTCTTCTAGAAGATGAACAGCAGACTGG	1057
QY	408	-----GlyLeuM	410
Db	1058	TGATAAGTACACACGACGACCAACCTTAAGTACTTCTGCCAGTGGCAGTCTGATTTGA	1117
QY	410	ecGlyLysAspGlyThrArgHisAspHisAlaIleLeuLeuThrGlyLeuAspIleCys	430
Db	1118	TGGGGAAGATGGGACTCGTCATGACCAAGCATCTTACTGACTGCTGTGATATATGTT	1177
QY	430	erTrpLysAsnGluProCysAspThrLeuGlyPheAlaProIleSerGlyMetCysSerL	450
Db	1178	CCTGGAAGAATGAGCCCTGTGACACTTTGGGATTTGGACCCCATTAAGTGAATGTAGTA	1237
QY	450	ysTyrArgSerCysThrIleAsnGluAspThrGlyLeuGlyLeuAlaPheThrIleAlaH	470
Db	1238	AATATCGCAGCTGCACGATTAATGAAGATACAGGCTCTTGACTGGCCTTCACCATTGCCC	1297
QY	470	IsGluSerGlyHisAsnPheGlyMetIleHisAspGlyGluGlyLysMetCysLysLys	490
Db	1298	ATGAGTCTGCACACAACCTTTGGCATGATTCATGATGAGAAGGGAACATGTTAAAAAGT	1357
QY	490	erGluGlyAsnIleMetSerProThrLeuAlaGlyArgAsnGlyValPheSerTrpSerP	510
Db	1358	CCGAGGGCAACATCATGTCCCTTACATTGGCAGAGACGCAATGAGTCTTCTCTGCTCAC	1417
QY	510	roCysSerArgGlnTyrLeuHisLysPheLeuSerThrAlaGlnAlaIleCysLeuAlaA	530
Db	1418	CTGCAGCCGCCAGTATCTACACAATAATTTCTAAGCACCCGCTCAAGCTATCTGCTGCTG	1477
QY	530	spGlnProLysProValLysGluTyrLysTyrProGluLysLeuProGlyGluLeuTyrA	550
Db	1478	ATCAGCCAAAGCCTGTGAAGGATACAAAGTATCTTGAGAAATTGCCAGGAAATTATATG	1537
QY	550	spAlaAsnThrGlnCysLysTrpGlnPheGlyGluLysAlaLysLeuCysMetLeuAspP	570
Db	1538	ATGCAAAACACAGGTGCAGGTGGAGAGAAAGCAAGCTCTGCATGCTGACT	1597
QY	570	helysLysAspIleCysLysAlaLeuTyrCysHisArgIleGlyArgLysCysGluThrL	590
Db	1598	TTAATAAAGACATCTGTAAAGCCCTGTGTGCATGTAATGGAAGAAATGTAGACTA	1657
QY	590	ysPheMetProAlaAlaGluGlyThrIleCysGlyHisAspMetTrpCysArgGlyGlyG	610
Db	1658	AATTTATGCCAGCAGCAGAAAGCACAAATTTGTGGCATGATGTGTGTGCGGGAGAGAC	1717

QY	610	INcysVallySTyrgLYaSPglUGLYpRoLYsProthrhISGLYhISetpSerAspTrpS	630
Db	1718	AGTGTGTGAATAATATGTGTGATGAAGGCCCAAGCCCAACCCATGGCCACTGTGGACTGTGT	1777
QY	630	erSerTrpSerProCYsSerArgrThrcYsGLYGLYGLYValSerhISaArgSerArgLeuc	650
Db	1778	CTTCTTGTGTCCCATGCTCTCCAGGACCTGTGGAGGGGGAGTATCTCATAGGAATCGCCTCT	1837
QY	650	ySThrAsnProLYsProSerhISGLYGLYLYsPheCYsGLUGLYSerThraTrgThrLeuL	670
Db	1838	GCAACCAACCCCAAGCCATCCCATGGAGGAAAGTTCTGTGAGGGGCTCCACTCGCACTCTGA	1897
QY	670	ySLeuCYaAsnSerGLInLYsCYsProArgrAspSerValaSPpheArGLaLaGLInCYsA	690
Db	1898	AGCTCTGCACACAGTCAGAAATGTCCCCGGGACAGTGTGACTTCCGTCTGCTCAAGTGTG	1957
QY	690	laGLuhiSaAsnSerArgrpPheArgrGLYArghISrLYsTrpLYsProTYrThrGLInY	710
Db	1958	CCGAGCACACACAGACGACGATTTCAGAGSGCGGCACTACAGTGAAGCCTTACACTCAAG	2017
QY	710	aGLuAspGLInaSPLeuCYeLYsLeuTYrCYsILealGLUGLYPheAspPhePhePheS	730
Db	2018	TAGAAGATCAGGACCTTATGCAAACTCTACTGTATCGCAGAAGGATTTGATTTCTTCTTT	2077
QY	730	erLeuSerAnLYsValLYsAspGLYThrProCYsSerGLuAspSerArgrAsnValCYsI	750
Db	2078	CTTGTGCAATAAAGTCAAGATGGGACTCCATGCTCGAGAGGATAGCCGTAATGTTGTGA	2137
QY	750	leAspGLYleCYsGLuArGLYGLYCYsAspAsnValleuGLYSerAspAlaValGLua	770
Db	2138	TAGATGGGATATGTGAGAGAGTTGAGTGTGACAATGTCTTGATCTGATGCTGTGAAG	2197
QY	770	spValCYeGLYValCYsAsnGLYAsnAsnSerAlaCYsThrILeHisArgGLYLeuTYrT	790
Db	2198	ACGTCTGTGGGGTGTGTAAACGGGAATACTCAGCCCTGCACGATTCAAGGGGTCTTACA	2257
QY	790	hrLYsHISHisThraSnGLInTYrThrHISMeValThrILeProSerGLYAlaArgS	810
Db	2258	CCAAGCACACACACACCAACCAAGTATATCACATGGTCAACCATTTCTTGAGCCCGGA	2317
QY	810	erILeArGLIeTYrGLuMeCAsnValSerThrSerTYrILeSerValArgAsnAlaLeua	830
Db	2318	GATCCGCACTTATGAATGAACGCTCTCACTCCTCATATTCTGTGGCAATGCCCTCA	2377
QY	830	rgArGLYrTYrLeuAsnGLYHISTrpThrValaSPTrpProGLYArGLYrLYsPheSerG	850
Db	2378	GAAGGTACTAAGTGAATGGGCACCTGGAACGTGACCTGGCCCGGCTGACAAATTTTCGG	2437
QY	850	LYThrThrPheAspTYrArgrArgSerTYrAsnGLuProGLuAsnLeuILealathrGLYp	870
Db	2438	GCACACTTTCGACTACAGACAGCGTCTTATATGAGCCCGAGAACTTAATCGCTACTGGAC	2497
QY	870	roThraSnGLuThrLeuILeValGLuLeuLeuPheGLInLYArgrAsnProGLYValaLaT	890
Db	2498	CAACCAACGAGACACTGATGTGTGAGCTGTCTTTCAAGGAAGAAACCCGGGTGTTCCT	2557
QY	890	rPLuTYrSerMetProArgrLeuGLYThrGLuLYsGLInProProalagInProSerTYrT	910
Db	2558	GGGAATACTCCATGCGCTCGCTTGGGACCGAGAAAGACCCCTGCCACGCCACGTACA	2617
QY	910	hrTrpAlaILeValArgSerGLuCYsSerValSerCYsGLYGLYArg	926
Db	2618	CTTGGGGCATCGTGGCTCTGTAGTGTCTCGTGTCTCTGGAGGGGGACAG	2667

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RESULT 3
US-09-930-872-5
; Sequence 5, Application US/09930872
; Patent No. 6448388
; GENERAL INFORMATION:
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Hilbun, Erin
; TITLE OF INVENTION: No. 6448388e1 Human Proteases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0219-USA

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; CURRENT APPLICATION NUMBER: US/09/930,872
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,852
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4042
; TYPE: DNA
; ORGANISM: homo sapiens
; US-09-930-872-5

Alignment Scores:
Pred. No.: 0          Length: 4042
Score: 3981.50       Matches: 764
Percent Similarity: 78.26%  Conservative: 17
Best Local Similarity: 76.55%  Mismatches: 38
Query Match: 76.04%      Indels: 181
DB: 3                  Gaps: 10

US-09-981-151D-8 (1-952) x US-09-930-872-5 (1-4042)

QY      1 MetLysPProARgAlaArgGlyTPARgGlyLeuAlaAlaLeuTPMetLeuAlaGln 20
DB      99 ATGAAGCCCCCGCGCGCGGATGCGGGGCTTGGCGCGCTGTGATGCTGCGCGCAG 158
QY      21 ValAlaGlnValSerProGlyArgSerHisGlnArgGlyAsnArgGlySerGlyGln 40
DB      159 GTGGCCGAGCA----- 169
QY      41 LeuGluAlaSerProProArgLeuLeuSerArgGlyProArgArgLeuThrAlaMetSer 60
DB      169 ----- 169
QY      61 ProLeuPheSerAlaGlyThrCysValArgHisGlyThrArgSerGlySerAlaTPGlu 80
DB      170 -----GGCACTTGCGTGGCCATGGGACCCGCGCGGCGGCGCTGGAG 214
QY      81 ProGluArgProAlaSerSerSerThrArgGlyAlaAlaGlyLeuAspGly-LysGlyAr 100
DB      215 CCCGAGCGTCCCGCGCTCTCTCTCCACCCGCGGAGCGGCGGCTGGATGGAAGGGC-- 272
QY      100 GAspMetAspGluAlaGlyAsnHisArgSerGlnGlnThrAsnThrGlyThrGluAsnGln 120
DB      272 ----- 272
QY      120 nThrLeuHisValLeuThrGlnTyrAspLeuValSerAlaTyrGluValAspHisArgGln 140
DB      273 -----GAAATATGACCTGGTCTCTGCTTACGAGGTGACCAAGGGG 313
QY      140 YAspTyrValSerHisGluIleMetCHisHisGlnArgArgArgAlaValAlaValSe 160
DB      314 CGATTACGTGTCCCATGAATCATGCAACCATCAAGCGGCGGAGAAAGACAGATGGCGTGT 373
QY      160 rGluValGluSerLeuHisLeuArgLeuLysGlyProArgHisAspPheHisMetAspLe 180
DB      374 CGAGGTGAGTCTTCTCACCTTGCGCTGAAAGGCTCCAGGCACGACTTCCACGTGATCT 433
QY      180 uArgThrSerSerSerLeuValAlaProGlyPheIleValGlnThrLeuGlyLysThrGln 200
DB      434 GAGGACTTCCAGCAGCCTAGTGGCTCTGCTTATTTGTGACAGCGTTGGAAAGACAGG 493
QY      200 YThrLysSerValGlnThrLeuProProGluAspPheCysPheTyrGlnGlySerLeuAr 220
DB      494 CACTAAGTCTGTGAGACTTATCCGCCAGAGGACTTCTGTTTATCAAGGCTCTTTGGCG 553
QY      220 gSerHisArgAsnSerProSerHisGlyGlyLysPheCysGlnGlySerThrArgThrLe 240
DB      554 ATCACACAGAAACTCC--TCAGTGGCCCTTTCAACCTGCCAAGGCTTGTCAAGCATGAT 610
QY      240 uLysLeuCysAsnSerGlnLysCysProArgAspSerValAspPheArgAlaAlaGlnCy 260
DB      611 ACGA-----ACAGAAGAGCAGATTACTTCTTAAGGCCACT 646
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QY      260 sAlaGluHisAsnSerArgArgPheArgGlyArgHisTyrLysTPLeuProTyrThrGln 280
DB      647 TCCTTCACACTCTCTCA-----TGAAA----- 668
QY      280 nValGluAlaAspLeuCysLysLeuTyrCysIle-AlaGlnGlyPheAspPhePheS 300
DB      669 -----CTGGCAGAG----- 678
QY      300 erLeuSerAsnLysValLysAspGlyThrProCysSerGluAspSerArgAsnValCysI 320
DB      679 --CTGCCAAGCAGCTCGCCATCCACGTACTGTACAGAAGATCCACAGAGCCCCATGC 736
QY      320 leAspGlyIleCysGluLeuSerValValSerThrSer-----AlaHis----- 334
DB      737 TCCT-GGGGCGAGTGAAGTCTGTGTGACCTCAAGACATGGAGCTGGCACATCAACCCC 795
QY      334 ----- 334
DB      796 TGACACAGCAGCAGCTTGGCTGGGACTGGCCACAAGAAGCAGATTCTGTGGAAGACGCA 855
QY      335 -----MetProGlnProProLysGluAspLeuPheIleLeuProAspGluTyrLys 352
DB      856 AGAATATACATGCCCGCGCTCCCAAGAAAGACCTTTCATCTTGGCCAGATGATTAAGT 915
QY      352 erCysLeuArgHisLysArgSerLeuLeuArgSerHisArgAsnGlnGluLeuAsnValG 372
DB      916 CTGCTTACGCGCATTAAGCGCTCTCTGTGAGGTCCCATAGAAATGAAGAATGAACGTGG 975
QY      372 LuThrLeuValValValAspLysLysMetMetGlnAsnHisGlyHisGluAsnIleThrT 392
DB      976 AGACCTTGGTGGTGTGTCGACAAAGAATGATGCAAAACCATGCGCCATGAATAATCACCA 1035
QY      392 hrTyrValLeuThrIleLeuAsnMetValSerAlaLeuPheLysAsp----- 407
DB      1036 CCTACGTGTCTACGATACTCAACATGTGATCTTATTCAAAAGATGAACAATAGAG 1095
QY      407 ----- 407
DB      1096 GAAACATCAACATTGCAATTGTAGTGTGATTCTTCTAGAAGATGAACAGCAGACTGG 1155
QY      408 -----GlyLeuM 410
DB      1156 TGATAAGTCAACACGACAGACCAACCTTAAGTAGCTTCTGCCAGTGGCAGTCTGGATTGA 1215
QY      410 etGlyLysAspGlyThrArgHisAspHisAlaIleLeuLeuThrGlyLeuAspIleCysS 430
DB      1216 TGGGGAAGAATGGGACTCGTCAATGACCAAGCCATCTTACTGACTGGTGTGATATATGTT 1275
QY      430 erTPLeuAsnGluProCysAspThrLeuGlyPheAlaProIleSerGlyMetCysSerL 450
DB      1276 CTTGAAGATGAGCCCTGTGACACTTTGGGATTTGCCACCAATAAGTGAATGTGTAGTA 1335
QY      450 ySTyrArgSerCysThrIleAsnGluAspThrGlyLeuGlyLeuAlaPheThrIleAlaH 470
DB      1336 AATATCGCAGCTGCACGATTAATGAAGATACAGGCTTGGACTGGCCTTCAACATTGGCCC 1395
QY      470 iSGluSerGlyHisAsnPheGlyMetIleHisAspGlyGlnGlyAsnMetCysLysLysS 490
DB      1396 ATGAGTCTGGACACAACTTTGGCATGATTCTGATGGAAGGAACATGTGTAAAGT 1455
QY      490 erGluGlyAsnIleMetSerProThrLeuAlaGlyArgAsnGlyValPheSerTrpSerP 510
DB      1456 CCGAGGCAACATCATGTCTCCCTACATTGGCAGGACGCAATGGAAGTCTTCTCGGTCTAC 1515
QY      510 roCysSerArgGlnTyrLeuHisLysPheLeuSerThrAlaGlnAlaIleCysLeuAlaA 530
DB      1516 CTTGCAAGCCGCAAGTATCTACAAATTTCTAAGCACCGCTCAAGCTATCTGCTTGTCTG 1575
QY      530 sPGLnProLysProValLysGluTyrLysTyrProGluLysLeuProGlyGluLeuTyrA 550
DB      1576 ATCAGCCAAAGCCTGTGAAGGAATACAAATATCTTGAAGAAATTGCCAGGAGAAATTATATG 1635
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QY 550 sPaLaAsnThrGlnCysLysTrpGlnPheGluLysAlaLysLeuCysMetLeuAsp 570
DB 1636 ATGCACAAACACAGTCGCAAGTGGCAGTTCCGAGAGAAAGCCAACTCTGCATGCTGCACT 1695
QY 570 heLysLYsAspIleCysLysAlaLeuTrpCysHisArgIleGlyArgLYsCysGluThrL 590
DB 1696 TTAATAAAGGACATCTGTAAAGCCCTGTGGTCGATCGTATGGAAAGAAATGTAGACTA 1755
QY 590 ySPHemETProAlaAlaGluGlyThrIleCysGlyHisAspMetTrpCysArgLYGlyG 610
DB 1756 AATTATGCGACGACGAGAAAGCAATTGTGGGCATGACATGTGTGCGCGGAGGAC 1815
QY 610 lncysValLysTyrgLYAspGluGlyProLYsProThrHisGlyHisITrPserAspTrps 630
DB 1816 AGTGTGTGAATATGTGTGATGAAGGCCCAAGCCCACTGATGCCACTGTGGACTGTGT 1875
QY 630 eRserTrpSerProCysSerArgTrpCysGlyGlyLYValSerHisArgSerArgLeuc 650
DB 1876 CTTCCTTGTCCTCCATGCTCCAGGACCTGCGGAGGGAGTACTCATAGAGATCGCCTCT 1935
QY 650 ySThrAsnProLYsProSerHisGlyLYLysPheCysGluGlySerThrArgThrLeul 670
DB 1936 GCACCAACCCCAAGCCATCGCATGGAGGAAGTTCTGTGAGGCTCCACTGCCACTCTGA 1995
QY 670 ySLeuCysAsnSerGlnLYsCysProArgAspSerValAspPheArgAlaAlaGlnCysA 690
DB 1996 AGCTCTGCAACAGTCAGAAATGTCCCGGGACAGTGTGACTTCGCTGCTCAGTGTG 2055
QY 690 lAGluHisAsnSerArgArgPheArgLYArgHisTYrLYsTrpLYsProTYrThrGlnV 710
DB 2056 CCGAGCACAAACAGACGACGATTCAGAGGCGGCACTACAAGTGAAGCCTTACACTCAAG 2115
QY 710 aLGlAspGlnAspLeuCysLysLeuTYrCysIleAlaGluGlyPheAspPhePhePhe 730
DB 2116 TAGAAGATCAGGACTTATGCAAACTCTACTGTATCGCAGAGGATTGATTCTTCTTTT 2175
QY 730 eRLeuSerAsnLYsValLYsAspGlyTYrProCysSerGluAspSerArgAsnValCysI 750
DB 2176 CTTTGTCAATTAAGTCAAGAGATGGGACTCCATGCTCGAGAGATAGCCGTAATGTTGTA 2235
QY 750 lEAspGlyIleCysGluArgValGlyCysAspAsnValLeuGlySerAspAlaValGluA 770
DB 2236 TAGATGGGATATGTGAGAGAGTGGATGTGACATGTCTTGATCTGATCTGTTGAAG 2295
QY 770 sPValCysGlyValCysAsnGlyAsnAsnSerAlaCysThrIleHisArgGlyLeuTYrT 790
DB 2296 ACGTCTGTGGGGTGTGTAAACGGGAATAACTGACCTGCACGATTCACAGGGGTCTTACA 2355
QY 790 hRLYsHisHisIsthAsnGlnTYrTYrHisMetValThrIleProSerGlyAlaArgS 810
DB 2356 CCAAGCACCAACCAACCAAGTATTATCATGTCAACCATTCCTTGTGAAGCCCGGA 2415
QY 810 eRlLeArgIleTYrGluMetAsnValSerThrSerTYrIleSerValArgAsnAlaLeuA 830
DB 2416 GTATCCGCACTATGAATGAACGTCTCTACTCTACATTTCTGTGCGCAATGCCCTCA 2475
QY 830 rGArgTYrTYrLeuAsnGlyHisITrPThrValAspTrpProGlyArgTYrLYsPheSerG 850
DB 2476 GAAAGTACTACTGAATGGGCACTGGAACCGGGAAGCTGGCCCGGTACAAATTTTCGG 2535
QY 850 lYThrThrPheAspTYrArgArgSerTYrAsnGluProGluAsnLeuIleAlaThrGlyP 870
DB 2536 GCACTACTTTCGACTACAGACGGTCTTATATGAGCCCGAGAACTTAATCGCTACTGAC 2595
QY 870 roThrAsnGluThrLeuIleValGluLeuLeuPheGlnGlyArgAsnProGlyValAlaI 890
DB 2596 CAACCAACGAGACACTGATGTGTGAGAGTGTGTTTTCAGGGAAGGAACCCGGGTGTGCT 2655
QY 890 rPGluTYrSerMetProArgLeuGlyTYrGluLYsGlnProProAlaGlnProSerTYrT 910
DB 2656 GGGATATCTCATGCTCGCTGGGGGACCGAGGAAGAGCCCTGCCACGACCACTACTACA 2715
QY 910 hRTrpAlaIleValArgSerGluCysSerValSerCysGlyGlyArg 926

DB 2716 CTTGGGCCATCGTGCCTCTGAGTGTCTCGTGTCTTCCGCGAGGGGAGACAG 2765
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US-10-217-774-5
; Sequence 5, Application US/10217774
; Patent No. 6734007
; GENERAL INFORMATION:
; APPLICANT: Fridde, Carl Johan
; TITLE OF INVENTION: No. 6734007e1 Human Proteases and Polynucleotides Encoding the
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0219-USA
; CURRENT APPLICATION NUMBER: US/10/217,774
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US/09/930,872
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,852
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4042
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-217-774-5
Alignment Scores:
Pred. No.: 0 Length: 4042
Score: 3981.50 Matches: 764
Percent Similarity: 78.26% Conservative: 17
Best Local Similarity: 76.55% Mismatches: 38
Query Match: 76.04% Indels: 181
DB: 4 Gaps: 10
US-09-981-151D-8 (1-952) x US-10-217-774-5 (1-4042)
QY 1 MetLYsProAlrGAlaArgLYTrpArgGlyLYLeuAlaAlaLeuTrpMetLeuLeuAlaGln 20
DB 99 ATGAAGCCCCCGCGCGCGGATGGCGGGGCTTGGCGGCTGTGATGCTGTGCGCGAG 158
QY 21 ValAlaGluGlnValSerProGlyArgSerHisGlnArgGlyAsnArgGlySerGlyGln 40
DB 159 GTGGCCAGCA----- 169
QY 41 LeuGluAlaSerProProArgLeuLeuSerArgLYProArgArgLeuThrAlaMetSer 60
DB 169 ----- 169
QY 61 ProLeuPheSerAlaGlyTYrCysValArgHisGlyTYrArgSerGlySerAlaTrpGlu 80
DB 170 -----GGCACCTGTGTCGCCATGGGACCCGACGGGACGGCTGGGAG 214
QY 81 ProGluArgProAlaSerSerSerThrArgGlyAlaAlaGlyLYLeuAspGly-LysGlyAr 100
DB 215 CCGGAGGCTCCCGCGCTCTCTCCACCCGCGAGCGGCGGGCTGATGGAAGGAGGC-- 272
QY 100 gAspMetAspGluAlaGlyAsnHisArgSerGlnGlnThrAsnThrGlyTYrGluAsnGln 120
DB 272 ----- 272
QY 120 nThrLeuHisValLeuThrGlnTYrAspLeuValSerAlaTYrGluValAspHisArgGly 140
DB 273 -----GAATATGACCTGTCTGTGCTTACGAGGTGACACAGGGG 313
QY 140 yAspTYrValSerHisGluIleMetHisHisGlnArgArgArgArgAlaValAlaValSe 160
DB 314 CGATTACGTGTCCCAATGAATCATGACCATGACGGCGGAGAAAGCACTGCGCGTGTCTC 373
QY 160 rGluValGluSerLeuHisLeuArgGlyLeuLYsGlyProArgHisAspPheHisMetAspLe 180
DB 374 CGAGTTGAGTCTTTCACCTTCGGGTGAAGGCTCCAGGACGACGACTTCCACGTGATCT 433

QY	180	uArgThrSerSerSerLeuValAlaProGlyPheIleValGlnThrLeuGlyLysThrG1	200
Db	434	GAGGACTTCCAGCAGCCTAGTGGCTTCTGGCTTTATTGTGCAGACGTTGGAAAGACAGG	493
QY	200	YThrLysSerValGlnThrLeuProProGluAspPheCysPheTyrglnGlySerLeuAr	220
Db	494	CACTAAGTCTGTGCACTTTACCGCCAGAGACTTCTGTTTCTATCAAGGCTCTTTGCG	553
QY	220	gSerHisArgAsnSerProSerHisGlyGlyLysPheCysGluGlySerThrArgThrLe	240
Db	554	ATCACACAGAAACTCC--TCAGTGGCCCTTTCAAACCTGCCAAGGCTTGTCAAGCATGAT	610
QY	240	uLysLeuCyAsnSerGlnLysCysProArgAspSerValAspPheArgAlaIaGlnCy	260
Db	611	ACGA-----ACAGAAAGGCGAGATTACTTCTTAAGGCCACT	646
QY	260	baIaGluHisAsnSerArgArgPheArgGlyArgHisTyrlYsTrPlySProTyThrG1	280
Db	647	TCCTTCACACCTCTCA-----TGGAAA-----	668
QY	280	nValGluAlaAspLeuCySlyLeuTyrcysIle-AlaGluGlyPheAspPhePheS	300
Db	669	-----CTGGCGAGAG-----	678
QY	300	erLeuSerAsnLysValLysAspGlyThrProCysSerGluAspSerArgAsnValCysI	320
Db	679	--CTGCCAAGGCAAGCTCGCCATCCACGTACTGTATCAAGAGATCCACAGAGCCCCATGC	736
QY	320	1eaSpGlyIleCysGluLeuSerValSerThrSer-----AlaHis-----	334
Db	737	TCCT-GGGGCCAGTGAAGTCTGTGTGACCTCAAGGACATGGAGCTGGACATCAACCCC	795
QY	334	-----	334
Db	796	TGCACAGCAGCGACCTTCGCTGGGACTGCCACAAAGCAGCAATTCTGTGAAGACGCA	855
QY	335	-----MetProGlnProProLysGluAspLeuPheIleLeuProAspGluTyrlYsS	352
Db	856	AGAAATACATGCCCCAGCCTCCCAAGAGAGACTTTCATCTTGCCAGATGATTAAGT	915
QY	352	erCysLeuArgHisLysArgSerLeuLeuArgSerHisArgAsnGluGluLeuAsnValG	372
Db	916	CTTGCTTACGGCAITAAAGCGCTCTCTTCTGAGGTCCCATAGAAATGAAGAACTGAACGTGG	975
QY	372	1uThrLeuValValValAspLysLysMetMetGlnAsnHisGlyHisGluAsnIleThrT	392
Db	976	AGACCTTGTGTGTGTCGACAAAGATGATGCAAAACCATGGCCATGMAAATATCACCA	1035
QY	392	hTyrlValLeuThrIleLeuAsnMetValSerAlaLeuPheLysAsp-----	407
Db	1036	CCTACGTGCTCAGATACTCAACATGGTATCTGCTTATTCAAGATGGAACATAGAG	1095
QY	407	-----	407
Db	1096	GAAACATCAACATTGCAATTGTAGGTCTGATTCTTCTAGAAGATGAACAGCAGGACTGG	1155
QY	408	-----GlyLeuM	410
Db	1156	TGATAAGTCACCAAGCAGACACACCTTAAGTAGCTTCTGCCAGTGGCAGTCTGATTGA	1215
QY	410	ecGlyLysAspGlyThrArgHisAspHisAlaIleLeuLeuThrGlyLeuAspIleCysS	430
Db	1216	TGGGGAAGATGGGACTCGTCATGACACAGCCCACTTACTGACTGGTCTGGATTATATGT	1275
QY	430	erTrpLysAsnGluProCysAspThrLeuGlyPheAlaProIleSerGlyMetCysSerL	450
Db	1276	CCTGGAAGATGAGCCCTGTGACACTTTGGGATTGACACCCATTAAGTGAATGTGTAGTA	1335
QY	450	yeTyrlArgSerCysThrIleAsnGluAspThrGlyLeuGlyLeuAlaPheThrIleAlaH	470
Db	1336	AAATATCGCAGCTGCACGATTAAATGAAGATACAGGCTTGTGACTGGCCTTACCACTTGGCCC	1395
QY	470	ieGluSerGlyHisAsnPheGlyMetIleHisAspGlyGluGlyAsnMetCysLysLys	490

Db	1396	ATGAGTCTGGACACAACTTTGGCATGATTCATGATGGAGAAGGAACATGTGTA AAAAGT	1455
QY	490	erGlYglYaaNIleMetSerProThrIleuAlaGlyArgAsnGlyValPheSerTrpSerP	510
Db	1456	CCGAGGGCAACATCATGTCTCCCTACATTTGGCAGGACGGCAATGGAGTCTTCTCGTGTCAC	1515
QY	510	roCysSerArgGlnTrpLeuHisLysPheLeuSerThrAlaGlnAlaIleCysLeuAlaA	530
Db	1516	CCTGCAGCCGCCAGTATCTAACACAATTTCTAAGCACCCGCTCAAGCTATCTGCCCTTGCTG	1575
QY	530	spGlnProLysProValLysGluTrpLysTyrProGlnLysLeuProGlyGluLeuTyrA	550
Db	1576	ATCAGCCAAAGCCTGTGAAGGAATACAGATATCCTGAGAAATTGCCAGAGAAATTATATG	1635
QY	550	spAlaAsnThrGlnCysLysTrpGlnPheGlyGluLysAlaLysLeuCysMetLeuAaP	570
Db	1636	ATGCAAAACACACAGTGCAGAGTGGCAGTTCGAGAGAAGAACCAAGCTCTGCATGCTGACT	1695
QY	570	helLysLysAspIleCysLysAlaLeuTrpCysHisArgIleGlyArgLysCysGluThrL	590
Db	1696	TTAAAAAGGACATCTGTAAAGCCCTGTGGTGCCATCTGATTTGGAAGAAATGTGAGACTA	1755
QY	590	ysPheMetProAlaAlaGluGlyThrIleCysGlyHisAspMetTrpCysArgGlyGlyG	610
Db	1756	AATTTATGCCAGCAGCAGACAGGACACAATTTGTGGGCATGACATGTGTGCGGGGAGGAC	1815
QY	610	lncYsValLysTyrGlyYaaPgluGlyProLysProThrHisGlyHisTrpSerAspTrpS	630
Db	1816	AGTGTGTGAATATGTGTATGAAGGCCCAAGCCCAAGCCCATGGCCACTGTCGAGCTGCT	1875
QY	630	erSerTrpSerProCysSerArgThrCysGlyGlyValSerHisArgSerArgLeuC	650
Db	1876	CTTCTTGTGTCCTCATGTCTCAGACCTGGGAGGAGGTATCTCATAGAGTGCCTCT	1935
QY	650	ysThrAsnProLysProSerHisGlyGlyLysPheCysGluGlySerThrArgThrLeuL	670
Db	1936	GCACCAACCCCAAGCCATGCATGGAGGAAAGTCTGTGAGGGCTCCACTCGCACTCGA	1995
QY	670	ysLeuCysAsnSerGlnLysCysProArgAspSerValAspPheArgAlaAlaGlnCysA	690
Db	1996	AGCTCTGCACACAGTCAGAAATGTCCCGGGACAGTGTGACTTCCGTGCTCAGTGTG	2055
QY	690	laGluHisAsnSerArgArgPheArgGlyArgHisTyrLysTrpLysProTyrThrGlnV	710
Db	2056	CCGAGCACACACAGCAGACGATTCAGAGGGCGGCACCTACAGTGGAAGCCTTACACTCAAG	2115
QY	710	alGluAspGlnAspLeuCysLysLeuTyrCysIleAlaGluGlyPheAspPhePhePheS	730
Db	2116	TAGAAGATCAGGACTTATGCCAACTCTACTGTATCGCGAAGAGATTGATTTCTTCTTT	2175
QY	730	erLeuSerAsnLysValLysAspGlyThrProCysSerGluAspSerArgAsnValCysI	750
Db	2176	CTTTGTCAAAATAAGTCAAAAGATGGGACTCCATGCTCGGAGGATAGCCGTAAATGTTGTA	2235
QY	750	leAspGlyIleCysGluArgValGlyCysAspAsnValLeuGlySerAspAlaValGluA	770
Db	2236	TAGATGGGATATGTGAAGAGATTGGATGTGACAATGTCTTGATCTGATGCTGTGAAG	2295
QY	770	spValCysGlyValCysAsnGlyAsnAsnSerAlaCysThrIleHisArgGlyLeuTyrT	790
Db	2296	ACGTCTGTGGGGTGTGTAAACGGGAATAACTCAGCCCTGCACGATTCAACAGGGGTCTTACA	2355
QY	790	hrLysHisHisThrAsnGlnTyrTyrHisMetValThrIleProSerGlyAlaArgS	810
Db	2356	CCAAGCACCAACACACCAACAGTATTAATCACATGGTCAACCATTTCTTCTGAGCCCCGA	2415
QY	810	erIleArgIleTyrGluMetAsnValSerThrSerTyrIleSerValArgAsnAlaLeuA	830
Db	2416	GTAATCCGACATCTATGAATGAACGTCTTAACCTCCATCATTTCTGTGCGCAATGCCCCA	2475
QY	830	rgArgTyrTyrLeuAsnGlyHisTrpThrValAspTrpProGlyArgTyrLysPheSerG	850

Db 2476 GAAGTACTACTGGAATGGGCACTGGACCGGTGCACTGGCCCGCGGTACAAATTTTCGG 2535
QY 850 lYThrThrpheaspTYrArgargSerTYrAsngluProgluAsnleuIlealathrGlyP 870
Db 2536 GCACTACTTTCGACTACAGACGGCTCTATATGAGCCCCGAGAACTTAATCGCTACTGGAC 2595
QY 870 roThrAsngluThrleuIleValgluLeuIleuPheGlnGlyAArgsnProglYValAlaT 890
Db 2596 CAACCAACGAGACACTGATTGTGAGCTGCTGTTTCAGGGAGAAACCCGGGTGTGCCT 2655
QY 890 rpgluTYrSerMetProArgleuGlyThrGluIysGlnProProAlaGlnProSerTYrT 910
Db 2656 GGGAACTACTCCATGCTCTCGCTTGGGGACCGAAGACAGCCCCCTGCCAGCCCACTACA 2715
QY 910 hrTPAlaIleValArgSerGluCysSerValSerCysGlyGlyArg 926
Db 2716 CTTGGCCATCGTGGCTCTGAGTGTCTCCGTCTCGGAGGGGACAG 2765

RESULT 5

US-09-930-872-1
; Sequence 1, Application US/09930872
; Patent No. 6448388
; GENERAL INFORMATION:
; APPLICANT: Fridde, Carl Johan
; APPLICANT: Hilbun, Erin
; TITLE OF INVENTION: No. 6448388el Human Proteases and Polynucleotides Encoding the Se
; FILE REFERENCE: LEX-0219-USA
; CURRENT APPLICATION NUMBER: US/09/930, 872
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225, 852
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1476
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-930-872-1

Alignment Scores:

Pred. No.:	3.31e-146	Length:	1476
Score:	1678.50	Matches:	359
Percent Similarity:	63.26%	Conservative:	18
Best Local Similarity:	60.23%	Mismatches:	40
Query Match:	32.06%	Indels:	181
DB:	3	Gaps:	10

US-09-981-151D-8 (1-952) x US-09-930-872-1 (1-1476)

QY 1 MetLysProArgAlaArgGlyTPArgGlyLeuAlaAlaLeuTrpMetLeuLeuAlaGln 20
Db 1 ATGAAGCCCCCGCGCGCGGATGGCGGGCTTGGCGCGCTGTGATGCTGTGGCGCAG 60
QY 21 ValAlaGluGlnValSerProglYArgSerHisGlnArgGlyAsnArgGlySerGlyGln 40
Db 61 GTGGCCGAGCA----- 71
QY 41 LeuGluAlaSerProProArgLeuLeuSerArgGlyProArgArgLeuThrAlaMetSer 60
Db 71 ----- 71
QY 61 ProLeuPheSerAlaGlyThrCysValArgHisGlyThrArgSerGlySerAlaTrpGlu 80
Db 72 -----GGCACCTGCGTGGCCATGGACCCGCGACGGCGACGGCCTGGAG 116
QY 81 ProGluArgProAlaSerSerSerThrArgGlyAlaAlaGlyLeuAspGly-LysGlyAr 100
Db 117 CCCGAGCGTCCCGCTCTCTCCACCCCGGAGCGCGCGCTGATGGAAGGAGC-- 174
QY 100 gAspMetAspGluAlaGlyAsnHisArgSerGlnGlnThrAsnThrGlyThrGluAsnG 120
Db 174 ----- 174

QY 120 nThrLeuHisValLeuThrGlnTYrAspLeuValSerAlaTYrGluValAspHisArgG 140
Db 175 -----GAATATGACTGTGTCTGCTTACGAGGTTGACACAGGGG 215
QY 140 YAspTYrValSerHisGlnIleMetHisHisGlnArgArgArgAlaValAlaValSe 160
Db 216 CGATTACGTGTCCATGAAATCATGACCATCAGCGGGGAGAAAGAGAGTGGCCGTGTC 275
QY 160 rGluValGluSerLeuHisLeuArgLeuLysGlyProArgHisAspPheHisMetAspLe 180
Db 276 CGAGGTGAGTCTTTCACCTTCGGCTGAAAGGCTCCAGGCACGACTTCCAGTGGATCT 335
QY 180 uArgThrSerSerSerLeuValAlaProGlyPheIleValGlnThrLeuGlyLysThrG 200
Db 336 GAGGACTTCCAGCAGCCTAGTGGCTCTGCTTATGTGACAGACGTTGGGAAAGACAGG 395
QY 200 YThrLysSerValGlnThrLeuProProgluAspPheCysPheTYrGlnGlySerLeuAr 220
Db 396 CACTAAGTCTGTGACAGACTTACCCGACAGAGACTTGTGTTCTATCAAGGCTTTGCG 455
QY 220 gSerHisArgAsnSerProSerHisGlyGlyLysPheCysGluGlySerThrArgThrLe 240
Db 456 ATCACACAGAAACTCC--TCAGTGGCCCTTTCACCTGCCAAGGCTTGTGACGATGAT 512
QY 240 uLysLeuCysAsnSerGlnLysCysProArgAspSerValAspPheArgAlaIaGlnCy 260
Db 513 ACGA-----ACAGAAAGGACGATTACTTCTTAAGGCCACT 548
QY 260 sAlaGluHisAsnSerArgArgPheArgGlyArgHisTYrLysTrpLysProtyrThrG 280
Db 549 TCCTTACACCTTCA-----TGAAA----- 570
QY 280 nValGluAlaAspLeuCysLysLeuTYrCysIle-AlaGluGlyPheAspPhePhePhe 300
Db 571 -----CTCGCAGAG----- 580
QY 300 erLeuSerAsnLysValLysAspGlyThrProCysSerGluAspSerArgAsnValCysI 320
Db 581 --CTGCCAAGGACGCTGCCATCCACGTACTGTACAAGAGATCCACAGACCCCATGC 638
QY 320 leAspGlyIleCysGluLeuSerValSerThrSer-----AlaHis----- 334
Db 639 TCCT-GGGGCGAGTAGGTCTGTGACCTCAAGACATGGAGCTGGCACATCAACCCC 697
QY 334 ----- 334
Db 698 TGACACAGCAGCACTTCGCTGGAGCTGCCAAMAAGCAGCATTTCTGTGAAGACGCA 757
QY 335 -----MetProGlnProProLysGluAspLeuPheIleLeuProAspGlyTYrLys 352
Db 758 AGAAATACATGCCCCAGCCTCCCAAGAAAGACCTTCATCTTGCCAGATGATATAGT 817
QY 352 erCysLeuArgHisLysArgSerLeuLeuArgSerHisArgAsnGluGluLeuAsnValG 372
Db 818 CTGCTTACGGCATAGCGCTCTCTGAGGTCCCATAGAAATGAGAATGAACGTGG 877
QY 372 luThrLeuValValAspLysLysMetMetGlnAsnHisGlyHisGluAsnIleThrT 392
Db 878 AGACCTGTGTGTGTGACAAATAATGATGCAAAACCATGGCCATGAATAATACACCA 937
QY 392 hrTYrValLeuThrIleLeuAsnMetValSerAlaLeuPheLysAsp----- 407
Db 938 CCTACGTGCTCAGATACTCAACATGTATCTGCTTATTCAAAAGATGAACAATAGAG 997
QY 407 ----- 407
Db 998 GAAACATCAACATTGCAATTGTAGTCTGATTCTTCTAGAAGATGAACAGCAGACTGG 1057
QY 408 -----GlyLeuM 410
Db 1058 TGATAAGTCACCAAGCAGACACACCTTAAGTAGCTTTCGACAGTGGCAGTCTGATTTGA 1117
QY 410 etGlyLysAspGlyThrArgHisAspHisAlaIleLeuLeuThrGlyLeuAspIleCys 430

DB 1118 TGGGGAAGATGGGACTCGTCATGACACGACCATTCTTACTGACTGGTCTGGATATATGTT 1177
QY 430 ERTPLYSASNGLUPROCYASBPThrLeuGlyPheAlaProIleSerGlyMetCysSerL 450
DB 1178 CTGGAGAAGATGAGCCCTGTGACACTTTGGGATTGGCACCCATTAAGTGAATGTGTAGTA 1237
QY 450 YSTYRARGSerCysThrIleASNGLUASBPThrGlyLeuGlyLeuAlaPheThrIleAlaH 470
DB 1238 AATATCGCAGCTGCACGATTAAATGAAGATACAGAGCTTGAGCTGGCTTCACCATTTGCC 1297
QY 470 IAGLUSerGlyHisASNpHeGlyMetIleHisASPGlyGlyLeuGlyASNMetCysLysLys 490
DB 1298 ATGAGTCTGACACAACTTTGGCATGATTGATGAGAGAAGGAACATGTGTAAGTA 1357
QY 490 ERGLUGlyASNleMetSerProThrLeuAlaGlyArgASNGLYValPheSerTrpSerP 510
DB 1358 CCGAGGGCAACATCATGTCCCTTACATTGGCAGAGACGCAATGAGTCTTCTCTGCTCAC 1417
QY 510 roCysSerArgGlnTyrLeuHisLysPheLeuSerThrAlaGln 524
DB 1418 CTGCAGCCGCGCATCTACACAAATTTCTAAGATCAGTGA 1461

RESULT 6

US-10-217-774-1
; Sequence 1, Application US/10217774
; Patent No. 6734007
; GENERAL INFORMATION:
; APPLICANT: Fridde, Carl Johan
; APPLICANT: Hilbun, Erich
; TITLE OF INVENTION: No. 6734007el Human Proteases and Polynucleotides Encoding the
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0219-USA
; CURRENT APPLICATION NUMBER: US/10/217,774
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US/09/930,872
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,852
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1476
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-217-774-1

Alignment Scores:

Pred. No.: 3,31e-146 Length: 1476
Score: 1678.50 Matches: 359
Percent Similarity: 63.26% Conservative: 18
Best Local Similarity: 60.23% Mismatches: 40
Query Match: 32.06% Indels: 181
DB: 4 Gaps: 10

US-09-981-151D-8 (1-952) x US-10-217-774-1 (1-1476)

QY 1 MetLysProARgAlaArgGlyTTPArgGlyLeuAlaAlaLeuTrpMetLeuLeuAlaGln 20
DB 1 ATGAAGCCCCCGCGCGCGGATGGCGGGCTTGGCGCGCGCTGTGATGCTGTGGCGCAG 60
QY 21 ValAlaGluGlnValSerProGlyArgSerHisGlnArgGlyASNArgGlySerGlyGln 40
DB 61 GTGGCCGAGCA----- 71
QY 41 LeuGluAlaSerProProArgLeuLeuSerArgGlyProArgArgLeuThrAlaMetSer 60
DB 71 ----- 71
QY 61 ProLeuPheSerAlaGlyThrCysValArgHisGlyThrArgSerGlySerAlaTrpGlu 80
DB 72 -----GGACCTTGCGTGGCGCCATGGGACCCGCGCGGCAAGCGCTGGAG 116

QY 81 ProGluArgProAlaSerSerSerThrArgGlyAlaAlaGlyLeuAspGly-LysGlyAr 100
DB 117 CCGGAGCGTCCCGCGCTCTCTCCACCCGCGGAGCGCGCGGCTGGATGGAAGAAGGC-- 174
QY 100 GAspMetAspGluAlaGlyASNHisArgSerGlnGlnThrASNThrGlyThrGluASNGL 120
DB 174 ----- 174
QY 120 nThrLeuHisValLeuThrGlnTyrAspLeuValSerAlaTyrGluValAspHisArgG 140
DB 175 -----GATATGACCTGGTCTTGCCTACGAGGTTGACCAAGGGG 215
QY 140 YAspTyrValSerHisGluIleMetHisHisGlnArgArgArgAlaValAlaValSe 160
DB 216 CGATTACGTGTCCTCATGAATCATGCACCATCAGCGCGGGAAGAAGACAGTGGCTGTC 275
QY 160 rGluValGluSerLeuHisLeuArgLeuGlyGlyProArgHisAspPheHisMetAspLe 180
DB 276 CGAGGTGAGTCTCTTCACTTCGGCTGAAGGCTCCAGGCAAGACTTCCACGTGATCT 335
QY 180 uArgThrSerSerSerLeuValAlaProGlyPheIleValGlnThrLeuGlyLysThrG 200
DB 336 GAGGACTTCCAGCAGCCTTAGTGCTCTGCTTATTGTGCAGACGTTGGGAAGAAGACAG 395
QY 200 YThrLysSerValGlnThrLeuProProGluAspPheCysPheTyrGlnGlySerLeuAr 220
DB 396 CACTAAGTCTGTGCAGACTTTACCGCCAGAGACTTCTGTTCATCAAGGCTCTTTGCG 455
QY 220 gSerHisArgASNserProSerHisGlyGlyLysPheCysGluGlySerThrArgThrLe 240
DB 456 ATCACACAGAAACTCC--TCAGTGGCCCTTCAACCTGCCAAGGCTTGTACAGCATGAT 512
QY 240 ulysLeuCysASNserGlnLysCysProArgAspSerValAspPheArgAlaAlaGlnCy 260
DB 513 ACGA-----ACAGAAGAGGACAGATTACTTCTTAAGGCCACT 548
QY 260 sAlaGluHisASNserArgArgPheArgGlyArgHisTyrLysTrpLysProTyrThrG 280
DB 549 TCCTTACACACTCTCA-----TGAAA----- 570
QY 280 nValGluAlaAspLeuCysLysLeuTyrCysIle-AlaGluGlyPheAspPhePhePhe 300
DB 571 -----CTGGCAGAG----- 580
QY 300 erLeuSerASNlysValLysAspGlyThrProCysSerGluAspSerArgASNValCysI 320
DB 581 --CTGCCCAAGGACGCTGCCATCCACGTAAGTGTACAGAAGATCCACAGAGCCCATGC 638
QY 320 leAspGlyIleCysGluLeuSerValValSerThrSer-----AlaHis----- 334
DB 639 TCCT-GGGGCAAGTGAAGTCTGTGACTCAAGACATGGAGAGCTGGCAGATCAACCCC 697
QY 334 ----- 334
DB 698 TGCACAGCAGGACCTTGGCTGGAGCTGCCACAAGACGACATTCTGTGAAGACGCA 757
QY 335 -----MetProGlnProProLysGluAspLeuPheIleLeuProAspGluTyrLys 352
DB 758 AGAATAATACATGCCCCAGGCTCCCAAGGAAGACCTTCAATCTTGCAGATGATTAAGT 817
QY 352 erCysLeuArgHisLysArgSerLeuLeuArgSerHisArgASNGLUleuASNValG 372
DB 818 CTGCTTACGCGCATTAAGCGCTCTCTGTGAGGTCCCATGAATGAAGACATGAACGTGG 877
QY 372 luThrLeuValValValAspLysLysMetMetGlnASNHisGlyHisGluASNleThrT 392
DB 878 AGACCTTGCGTGGTGCACAAAAGATGATGCAAAAACCATGGCCATGAATAATACCA 937
QY 392 hrTyrValLeuThrIleLeuASNMetValSerAlaLeuPheLysAsp----- 407
DB 938 CTTAGTGTCAAGATACATCATGTGTCTTATTTCAAAAGATGAACAATAGAG 997
QY 407 ----- 407

Db 998 GAAACATCAACATTGCATTGTAGTCTGATTCTTTAGAGATGAACAGCCAGACTGG 1057
QY 408 -----GlyLeuM 410
Db 1058 TGATAAGTACCAACGACGACCACTTAAGTACTTTCGCCAGTGGCAGCTCGATTGA 1117
QY 410 etGlyLysAspGlyThrArgHisAspHisAlaIleLeuLeuThrGlyLeuAspIleCys 430
Db 1118 TGGGGAAGATGGGACTCGTCATGACACGCCACTTACTGACTGCTGTGATATATGTT 1177
QY 430 eRTTrpLysAsnGluProCysAspThrLeuGlyPheAlaProIleSerGlyMetCysSerL 450
Db 1178 CCTGGAAGATGAGCCCTGTGACACTTTGGGATTGGACCCATAAGTGAATGTGTAGTA 1237
QY 450 yRTYrArgSerCysThrIleAsnGluAspThrGlyLeuAlaPheThrIleAlaH 470
Db 1238 AATATCGCAGCTGCACGATTATGAAGATACAGGCTTGGACTGGCCTTCACCATTTGCC 1297
QY 470 iRGluSerGlyHisAsnPheGlyMetIleHisAspGlyGlyGlyAsnMetCysLysLys 490
Db 1298 ATGAGTCTGGACACAACCTTTGGCATGATTCATGATGGAAGGGAACATGTGTAAAAAGT 1357
QY 490 eRGluGlyAsnIleMetSerProThrLeuAlaGlyArgAsnGlyValPheSerTrpSerP 510
Db 1358 CCGAGGGCAACATCATGTCCCTTACATTGGCGAGACGCAATGAGTCTTCTCTGCTCAC 1417
QY 510 rOCysSerArgGlnTyrLeuHisLysPheLeuSerThrAlaGln 524
Db 1418 CCTGCAGCCGCCAGTATCTACACAATTCTTAAGATCAGTGAAA 1461

RESULT 7

US-09-963-791-1

; Sequence 1, Application US/09963791

; Patent No. 6649399

; GENERAL INFORMATION:

; APPLICANT: Donoho, Gregory

; APPLICANT: Turner, C. Alexander Jr.

; APPLICANT: Friedrich, Glenn

; APPLICANT: Scoville, John

; APPLICANT: Zambrowicz, Brian

; APPLICANT: Sands, Arthur T.

; TITLE OF INVENTION: No. 6649399e1 Human Proteases and Polynucleotides Encoding the Sa

; FILE REFERENCE: LEX-0105-USA

; CURRENT APPLICATION NUMBER: US/09/963,791

; PRIOR APPLICATION NUMBER: 2000-12-08

; PRIOR FILING DATE: 1999-12-09

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: FastSeq for windows Version 4.0

; SEQ ID NO 1

; LENGTH: 2727

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-09-963-791-1

Alignment Scores:

Pred. No.:	7.03e-119	Length:	2727
Score:	1390.00	Matches:	313
Percent Similarity:	49.18%	Conservative:	137
Best local Similarity:	34.21%	Mismatches:	294
Query Match:	26.55%	Indels:	172
DB:	4	Gaps:	25

US-09-981-151d-8 (1-952) x US-09-963-791-1 (1-2727)

QY 108 HisArgSerGlnGlnThrAsnThrGlyThrGluAsnGlnThrLeuHisValLeuThrGln 127
Db 64 CATAGTGACCAACAGGCTTTCATACAGTTCGAAGAAATTCCTGACTTATCTTGAACAC 123
QY 128 TyrAspLeuValSerAlaTyrGluValAspHisArgGlyAspTyrValSerHisGluIle 147
Db 124 TACCAGCTACTATTCCAATGAAGGTGATCAAAATGAGCATTTCTACGCTTTACTGTG 183

QY 148 MeChis-----HisGlnArgArgArgAlaVal-----AlaValSerGlu 161
Db 184 AAAAATGATAAACACTCAAGAGAGAGAGAGAGATATGACCCCTATTGATCCACAGACGCA 243
QY 162 ValGluSerLeuHisLeuArgLeuLysGlyProArgHisAspPheHisMetAspLeuArg 181
Db 244 GTATCTAAGTATTATTTTAAACTTTCACGCTATGGCAACACTTTCATCTTAAACTTGACT 303
QY 182 ThrSerSerSerLeuValAlaProGlyPheIleValGlnThrLeuGlyLysThrGlyThr 201
Db 304 CTCACACAGATTGTGTGCCAAACATTTTACAGTAGAATATTGGGGGAAAGATGGA--- 360
QY 202 LysSerValGlnThrLeuProProGlu-----AspPheCysPheTyr 215
Db 361 -----CCCCAGTGAACATGATTTTGTAGACAACTGTCTATTAC 399
QY 216 GlnGlySerLeuArgSerHisArgAsnSerProSerHisGlyGlyLysPheCysGluGly 235
Db 400 ACAGGATATTTCACAGATCAACGATGACACTAAAGTGGCTTTAAGCAACTGTGTGGG 459
QY 236 SerThrArgThrLeuLysLeuCysAsnSerGlnLysCysProArgAspSerValAspPhe 255
Db 460 TTGCATGGCTTATT----- 474
QY 256 ArgAlaAlaGlnCysAlaGlnHisAsnSerArgArgPheArgGlyArgHisTyr----- 273
Db 475 ---GCTACAGAAGATGAAGATATT-TATGAACTTTTAAAGAAATACACAGAGATTTC 530
QY 274 -----LysTrpLysProTyrThrGlnValGluAlaAspLeuCysLys 287
Db 531 CAAGCATTTTAGTTATGTAATAATGGCCACC-----TCATGTTAT 569
QY 288 LeuTyrCysIleAlaGlu-----GlyPhe 295
Db 570 TTACAAAAGTCTGCCCTTCAACAAGACATCTGTATGATCACTCTCATTTGGGGTTTC 629
QY 296 -AspPhePhePheSerLeuSerAsnLysValLysAspGlyThrPro---CysSerGluAs 314
Db 630 GGATTTTC-----ACAAGAAGTGGCAAAACCTTGGTGGCTGAATGA 668
QY 314 pSerArgAsnValCysIleAspGlyIleCysGluLeuSerValValSerThrSerAlaHis 334
Db 669 CACATCCACTGTTTCTTAT-----TCACTACCAATTAAACACACACATATGCCA 716
QY 334 sMetProGlnProProLysGluAspLeuPheIleLeuProAspGluTyrLysSerCysLe 354
Db 717 CCAC----- 720
QY 354 uArgHisLysArgSerLeuLeuArgSerHisArgAsnGluGluLeuAsnValGluThrLe 374
Db 721 -AGACAGAAAGATCAGTGTG-----AGCATTGAACGGTTTGTGAGACATT 764
QY 374 uValValValAspLysLysMetMetGlnAsnHisGlyHisGluAsnIleThrThrTyrVa 394
Db 765 GGTAGTGGCAGACAAATGATGTGGGCTACCATGGCCGCAAGACATTGAACATTACAT 824
QY 394 lLeuThrIleLeuAsnMetValSerAlaLeuPheLysAspGlyLeuMetGly----- 411
Db 825 TTTGAGTGTGATGAATATGTGTGCCAAACTTACCGTGATTCAGCCTGAGAAACGTTGT 884
QY 411 ----- 411
Db 885 GAATATTATAGTGCCCGCTTAATGTCTCACAGAGATCAGCCAACTTGAGATATAA 944
QY 411 ----- 411
Db 945 CCACCATGACAGACAAGTCCCTCGATAGCTTCTGTAATGGCAGAAATCCATTCTCTCCCA 1004
QY 412 ----LysAspGly-----ThrArgHisAspHisAlaIle 422
Db 1005 CCAAGTGTATGAAACACCATTCAGAAATGGGATGGCCACACGATTAATGACAGTTCT 1064

QY	422	uLeuThrGlyLeuAspIleCysSerTrpLysAsnGluProCysAspThrLeuGlyPheAl	442
Db	1065	TATTACTAGATATGATATCTGCACCTTATATAAAATAAAGCCCTGTGGAAACACTGGGCTTGGC	1124
QY	442	aProIleSerGlyMetCysSerLysTyrArgSerCysThrIleAsnGluAspThrGlyLe	462
Db	1125	CTCTGTGGCTGGTAATGTGTGAGCCTGAAAGGAGCTGCAGCATTTAATGAAGACATTGGCCT	1184
QY	462	uGlyLeuAlaPheThrIleAlaHisGluSerGlyHisAsnPheGlyMetIleHisAspGl	482
Db	1185	GGGTTCAAGCTTTTACCATTGTCACATGAGATTGGTCACAATTTGGTATGAACCATGATGG	1244
QY	482	yGluGlyAsnMetCys-----LysLysSerGlu--GlyAsnIleMetSerProThrLe	499
Db	1245	AATTGGAATTTCTTGTGGAGCAAGGTCATGAAGCAGCAAAACTTATATGGCAGCTCACAT	1304
QY	499	uAlaGlyArgAsnGlyValPheSerTrpSerProCysSerArgGlnTyrLeuHisLysPh	519
Db	1305	TACTGCGAATACCAATCCTTTTCTGCTGCTGCTTGACGTGAGACTACATCACCACTT	1364
QY	519	eLeuSerThrAlaGlnAlaIleCysLeuAlaAspGlnProLysProValLysGluTyrLy	539
Db	1365	TCTAGATTCAAGCCGTGGTACTTGCCTTGATATAGACCT--CCCAAGCGTGACTTTCT	1421
QY	539	sTyrProGluLysLeuProGlyGluLeuTyrAspAlaAsnThrGlnCysLysTrpGlnPh	559
Db	1422	TTATTCAGCTGTGGCCCGCAGGTCAAGTGTATGATGCTGATGAGCAATGTGTTTCCAGTA	1481
QY	559	eGlyGluLysAlaLysLeuCysMetLeuAspPheLysLysAspIleCysLysAlaLeuTr	579
Db	1482	TGGAGCAACCTCCCGCAATGTAAATATAGG-----GAAGTGTAGAGAGCTCTG	1532
QY	579	pCysHisArgIleGlyArgLysCysGluThrLysPheMetProAlaAlaGluGlyThrIl	599
Db	1533	GTGTCACAGCAAAAGCAACCGCTGTGTCCACCAACAGTATTCACAGACTGAGGGGACACT	1592
QY	599	eCysGly-----HisAspMetTrpCysArgGlyGlnCysValLysTyrGl	615
Db	1593	GTGTCAAACTGGGAATATTGAAAAAGGTGTGTATTACAGGAGATTGTGTTCTTTTG	1652
QY	615	yAspGluGlyProLysProThrHisGlyHisTrpSerAspTrpSerSerTrpSerProCy	635
Db	1653	C---ACTGGCCCCAGACATAGATGGGGGCTGGGGCTCCCTGCTCACTATGGGAGAGTG	1709
QY	635	sSerArgThrCysGlyGlyGlyValSerHisArgSerArgLeuCysThrAsnProLysPr	655
Db	1710	CAGCAGGACCTGGGGGAGGCGCTCTCATCCCTTAAGACACTGTGACAGTCCAGCACCC	1769
QY	655	oSerHisGlyGlyLysPheCysGluGlySerThrArgThrLeuLysLeuCysAsnSerGl	675
Db	1770	TTTCAGGAGGTGGAATATATTGCTTGGGGAAAGGAAACGGTATCGCTCCTGTAAACACA	1829
QY	675	nLysCysProArgAspSerValAspPheArgAlaAlaGlnCysAlaGluHisAsnSerAr	695
Db	1830	TCCATGCCCTTTGGGGTTCCCGAGATTTTCGAGAGAAACAGTGTGCAGACTTTGACAAATAT	1889
QY	695	gArgPheArgGlyArgHisTyrLysTrpLysProTyrThrGlnValGluAspGlnAspLe	715
Db	1890	GCCTTTCGAGGAAAGTATTATTAACCTGAAACCCTTACTGGAGGTGGGGTAAACCT--	1947
QY	715	uCysLysLeuTyrCysIleAlaGluGlyPheAspPhePhePheSerLeuSerAsnLysVa	735
Db	1948	-TGTGCATTAAACTGCTTGGCTGAAGGTATATAATTTCTACACTGAACGTGCTCTCGGCT	2006
QY	735	lLysAspGlyThrProCysSerGluAspSerArgAsnValCysIleAspGlyIleCysGl	755
Db	2007	GATCGATGGGACCCAGTGCAAATGGCGAATTCACCTGGAATATCTGCATCAATGAGAAATGCAA	2066
QY	755	uArgValGlyCysAspAsnValLeuGlySerAspAlaValGluAspValCysGlyValCy	775
Db	2067	GCACTAGGCTGTGATATAATTTTGGGATCTGATGCTAGGGAGATAGATGTGAGTCTG	2126
QY	775	sAsnGlyAsnAsnSerAlaCysThrIleHisArgGlyLeuTyrThrLysHisHisIsth	795

Db	2127	TGGAGGGGACGGAAGCACATGTGATGCCATTGGAAGGGTCTTCAATGATTCACCTGCCAG	2186
Qy	795	rasnglnIyTyrHismetValThrIleProserGlyalaArgserIleargIleTyrgI	815
Db	2187	GGGAGGCTACATGGAAGTGGTGCAGATACCAAGAGGCTCTGTTCACATTGAAGTTAGAGA	2246
Qy	815	uMetasnValSerThrSerTyriIeserValaArgasnAlaIeuArgargTyrrTyrlleuAs	835
Db	2247	AGTTGCCATGTCGAAGAACTATATTGCTTTAAATCTGGAAGAGATGATTAATATATA	2306
Qy	835	nglyHisTrpThrValasptTrpProglyArgTyrllysPheSerGlyThrThrPheasptly	855
Db	2307	TGGTGCCTTGACATATTGACTGGCCCTAGGAATTTGATGTTGCTGGGACACCTTTTCATT	2366
Qy	855	rArgargSerTyrrAsnGluProGluAsnIleuIlealathrglyProthrasnGluThrIle	875
Db	2367	CAAGAGACCAACTGATGAACCAAGATCCTTGGAAGCTCTAAGTCTCCTACCTCAGAAAATCT	2426
Qy	875	uIleValGluLeuIeuPheGlnGlyArgasnProGlyValAlaIatPrgluTyrrSerMetPr	895
Db	2427	CATGTCATAGGTTCTGCTTCAAGAACAGAAATTTGGGAATTAGGTATAGTTCATATGTTCC	2486
Qy	895	o-----ArgleuGlyThrGluIuLysGlnProAlaGlnProSerTyrrThrTrpAlaI	913
Db	2487	CATCACTGCAACTGGCAGTGGAGATAAAT-----GAAGTTGGCTTTACATGAATCA	2537
Qy	913	evalArg---SergluCysSerValSerCysGlyGlyArg	926
Db	2538	TCAGCCTTGCTCAGAAATGCTCAGCTACTGTGCTGAGAGTAAG	2580

```

RESULT 8
US-09-963-791-23
; Sequence 23, Application US/09963791
; Patent No. 6649399
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Scoville, John
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6649399el Human Proteases and Polynucleotides Encoding the Sam
; FILE REFERENCE: LEX-0105-USA
; CURRENT APPLICATION NUMBER: US/09/963,791
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 60/169,769
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 2274
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-963-791-23

Alignment Scores:
Pred. No.: 2.13e-112 Length: 2274
Score: 1319.00 Matches: 257
Percent Similarity: 57.26% Conservative: 106
Best Local Similarity: 40.54% Mismatches: 195
Query Match: 25.19% Indels: 76
DB: 4 Gaps: 13

US-09-981-151D-8 (1-952) x US-09-963-791-23 (1-2274)
QY 355 ArghIlysaRgSerleuLeuARgSerHIsARgAsnGLuLeuAsnValGIuThrLeu 374
||| ||||| ||||| ::| ||| ||||| |||||
Db 268 AGACAGAAAGATGATG-----AGCATTTGAACGGTTGTGTGAGACATTG 312

375 ValValValAspLylyMetMetClnAsnHIsGLyHIsGLuAsnIleThrTyrVal 394
||||| ||||| ||||| ||||| ||||| ||||| |||||
313 GTAGTGGCAGACAAATGATGTGTGGGCTTACCATGGCCGCAAGACATTGAACATTACATT 372

```

```
QY 395 LeuThrIleLeuAsnMetValSerAlaLeuPheLysAspGlyLeuMetGly----- 411
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 373 TTGAGTGTGATGAAATATGTGTGCCAAACTTTACCGTGATTCACGCCCTAGAAACGTTGTG 432
QY 411 ----- 411
Db 433 AATATTATAGTGGCCCGCTTAATTGTCTCACAGAAAGATCAGCCAACTTGAGATAAAC 492
QY 411 ----- 411
Db 493 CACCATGACAGACAAGTCCCTCGATAGCTTCTGTAATGGCAGAAATCCATTCTCTCCAC 552
QY 412 ---LysAspGly-----ThrArgHisAspHisAlaIleLeu 422
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 553 CAAAGTGATGGAAACACCATTCAGAAATGGGATGGCCACCAACGATAATGCACTTCTT 612
QY 423 LeuThrGlyLeuAspIleCysSerTrpLysAsnGluProCysAspThrLeuGlyPheAla 442
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 613 ATTAAGTATGATGATATCTGCACCTTATAAAATAAGCCCTGTGGAACACTGGGCTTGCC 672
QY 443 ProIleSerGlyMetCysSerLysTrpArgSerCysThrIleAsnGluAspThrGlyLeu 462
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 673 TCTGTGCTGGATGTGTGAGCCTGAAAGAGCTGCAGCATTAATGAAGACATTGGCCCTG 732
QY 463 GlyLeuAlaPheThrIleAlaHisGluSerGlyHisAsnPheGlyMetIleHisAspGly 482
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 733 GGTTCAGCTTTTACCATTCATTCACATGAGATTGGTCACAATTGGTATGAACCATGATGA 792
QY 483 GluGlyAsnMetCys-----LysLysSerGlu---GlyAsnIleMetSerProThrLeu 499
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 793 ATTGGAATTTCTTGTGGAGCAGAAAGTCATGAAGCAGCAAACTTATGGCAGCTCACATT 852
QY 500 AlaGlyArgAsnGlyValPheSerTrpSerProCysSerArgGlnTrpLeuHisLysPhe 519
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 853 ACTGCGAATACCAATCCTTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 912
QY 520 LeuSerThrAlaGlnAlaIleCysLeuAlaAspGlnProLysProValLysGluTrpLys 539
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 913 CTAGATTCAAGCCGTGGTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 969
QY 540 TyrProGluLysLeuProGlyGluLeuTyrAspAlaAsnThrGlnCysLysTrpGlnPhe 559
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 970 TATCCAGCTGTGGCCCCCAGGTGAGGTGATGATGATGATGATGATGATGATGATGATGAT 1029
QY 560 GlyGlyLysAlaLysLeuCysMetLeuAspPheLysLysAspIleCysLysAlaLeuTrp 579
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 1030 GAGACCACTCCCGCCAATGTAAATATGG-----GAAGTGTGTAGAGAGCTCTGG 1080
QY 580 CysHisArgIleGlyArgLysCysGluThrLysPheMetProAlaAlaGluGlyThrIle 599
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 1081 TGTCTCAGCAAAAGCAACCGCTGTGTCAACCAAGTATTCAGCAGCTGAGGGGACACTG 1140
QY 600 CysGly-----HisAspMetTrpCysArgGlyGlnCysValLysTyrGly 615
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 1141 TGTCAAACTGGGAATATTGAAAAAGGGTGTGTATCAGGGAGATTGTGTTCTTTGGC 1200
QY 616 AspGluGlyProLysProThrHisGlyHisTrpSerAspTrpSerSerTrpSerProCys 635
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 1201 ---ACTTGGCCCCAGACATAGATGGGGCTGGGGTCCCTGCTCACTATGGGAGAGTGC 1257
QY 636 SerArgThrCysGlyGlyGlyValSerHisArgSerArgLeuCysThrAsnProLysPro 655
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 1258 AGCAGGACCTGGGGGGGAGGGCTCTCTCATCCCTTAAGACACTGTGACAGTCCAGCACCT 1317
QY 656 SerHisGlyGlyLysPheCysGluGlySerThrArgThrLeuLysLeuCysAsnSerGln 675
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 1318 TCAGGAGGTGAAAAATATTGCTCTGGGGAAGAAACGGTATCGCTCTGTAAACACAGAT 1377
QY 676 LysCysProArgAspSerValAspPheArgAlaAlaGlnCysAlaGlnHisAsnSerArg 695
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 1378 CCATGCCCTTTGGGTTCCCGAGATTTTTCGAGAGAAAACAGTGTGCAGACTTTGAACAATATG 1437
```

```
QY 696 ArgPheArgGlyArgHisTyrLysTrpLysProTyrThrGlnValGluAspGlnAspLeu 715
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 1438 CTTTCCGAGGAAAGTATTATACTGGAACCCCTATACTGGAGGTGGGTAACCT--- 1494
QY 716 CysLysLeuTyrCysIleAlaGluGlyPheAspPhePheSerLeuSerAsnLysVal 735
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 1495 TGTGATTAAACTGTGCTGAGAGGTATTAATTTCTACACTGAACGTGCTCTGGCGTG 1554
QY 736 LysAspGlyThrProCysSerGluAspSerArgAsnValCysIleAspGlyIleCysGlu 755
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 1555 ATGATGGACCCAGTGAATGCGGATTCACCTGATATCTGCATCAATGGAATGCAAG 1614
QY 756 ArgValGlyCysAspAsnValLeuGlySerAspAlaValGluAspValCysGlyValCys 775
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 1615 CACGTAGGCTGTGATTAATTTTGGGATCTGATGCTAGGGAAGATGATGCGAGTCTGT 1674
QY 776 AsnGlyAsnAsnSerAlaCysThrIleHisArgGlyLeuTyrThrLysHisHisThr 795
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 1675 GGAGGGGACGGAAGACATGTGATGCCATTGAAGGGTTCTCAATGATTCACCTGCCAGG 1734
QY 796 AsnGlnTyrTrpHisMetValThrIleProSerGlyValaArgSerIleArgIleTyrGlu 815
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 1735 GGAGGCTACATGGAAGTGTGACAGATACCAAGAGGCTGTTCAATGTAAGTAGAGAA 1794
QY 816 MetAsnValSerThrSerTyrIleSerValArgAsnAlaLeuArgArgTyrTrpLeuAsn 835
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 1795 GTTGCCATGTCAAGAAGTATATGTGTTAAATCTGAAGAGATGATTAATATTAAT 1854
QY 836 GlyHisTrpThrValAspTrpProGlyArgTyrLysPheSerGlyThrThrPheAspTyr 855
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 1855 GGTGCTGACTATTGACTGGCCTAGGAATTGATGTGCTGGAGAGCTTTTCATTAC 1914
QY 856 ArgArgSerTyrAsnGluProGluAsnLeuIleAlaThrGlyProThrAsnGluThrLeu 875
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 1915 AAGAGACCACTGATGAACAGAACTCTTGAAGCTTAGTCTTACCTCAGAAAATCTC 1974
QY 876 IleValGluLeuLeuPheGlnGlyArgAsnProGlyValAlaTrpGluTyrSerMetPro 895
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 1975 ATGTCATGTTCTGTCTTCAAGAACAGAAATTGGGAATTAGTATAGTTCAATGTTCCC 2034
QY 896 -----ArgLeuGlyThrGluLysGlnProProAlaGlnProSerTyrThrTrpAlaIle 913
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 2035 ATCACTGCAACTGACGTGGAGATTAAT-----GAAGTGTGCTTAATGATGATCAT 2085
QY 914 ValArg---SerGluCysSerValSerCysGlyGlyArg 926
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 2086 CAGCCTGTGTCAGAAATGCTCAGCTACTTGTGCTGAGGTAAAG 2127

RESULT 9
US-09-963-791-25
; Sequence 25, Application US/09963791
; Patent No. 6649399
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Scoville, John
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6649399e1 Human Proteases and Polynucleotides Encoding the San
; FILE REFERENCE: Lex-0105-USA
; CURRENT APPLICATION NUMBER: US/09/963,791
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 60/169,769
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 3160
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-963-791-25
```

Alignment Scores:

Pred. No.:	6.77e-109	Length:	3160
Score:	1284.00	Matches:	322
Percent Similarity:	44.60%	Conservative:	136
Best Local Similarity:	31.35%	Mismatches:	298
Query Match:	24.52%	Indels:	273
DB:	4	Gaps:	30

US-09-981-151D-8 (1-952) x US-09-963-791-25 (1-3160)

```
QY      108 HieArgSerGlnGlnThrAsnThrGlyThrGluAsnGlnThrLeuHisValLeuThrGln 127
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB      85 CATAGTGACCACAGCGCTTCATACAGTCTCTCAAGAGGAATTCCTGACTTATCTGAACAC 144

QY      128 TyrAspLeuValSerAlaTyrGluValAspHisArgGlyAspTyrValSerHisGluIle 147
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB      145 TACCAAGCTAACTATCCATTAAGGTTGATCAAAATGAGCATTTCTCAGCTTTACTGTG 204

QY      148 MetHis-----HisGlnArgArgArgAlaVal-----AlaValSerGlu 161
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB      205 AAAAATGATAACACTCAAGAGAGAGAGAGAGATGGAACCCCTATTGATCCACAGCAGCA 264

QY      162 ValGluSerLeuHisLeuArgLeuGlyGlyProArgHisAspPheHisMetAspLeuArg 181
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB      265 GTATCTAAGTTATTTTAACTTTCAGCCCTATGGCAAGCATTTCATCTAACTTGACT 324

QY      182 ThrSerSerSerLeuValAlaProGlyPheIleValGlnThrLeuGlyLysThrGlyThr 201
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB      325 CTCACACACAGATTTTGTGTCCAAACATTTTACAGTAAATATGGGGGAAAGATGGA--- 381

QY      202 LysSerValGlnThrLeuProGlu-----AspPheCysPheTyr 215
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB      382 -----CCCAAGTGGAACATGATTTTGAACAACCTGTCAATTAC 420

QY      216 GlnGlySerLeuArgSerHisArgAsnSerProSerHisGlyGlyLysPheCysGluGly 235
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB      421 ACAGGATATTGCAAGATCAACGTAAGTACAACTAAAGTGCGTTTAAGCAACTGTGTGGG 480

QY      236 SerThrArgThrLeuLysLeu-----CysAsnSerGlnLysCysProArgAspSer 252
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB      481 TT-GGAAAAGCTGCCAAAATTTTCTCTGCTGCAATTCA----- 518

QY      253 ValAspPheArgAlaAlaGlnCysAlaGlnHisAsnSer----- 265
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB      519 ---AGTTGGCTGGGGCGGAATTTGAAGTGAAGAAACGATGGTGTATTGCTACAGAAAG 575

QY      266 -----ArgArgPheArgGlyArgHisTyr----- 273
      |||  |||  |||  |||  |||  |||  |||  |||  |||
DB      576 TGAAGAGTATTTTATCGAACCTTTAAAGAAATACACAGAGATTCGAAGCATTTTAGTTA 635

QY      274 ---LysTrpLysProTyrThrGlnValGluAlaAspLeuCysLysLeuTyrCysIleAla 292
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB      636 TGAATAATGCCACCC-----TCATGTATTTCAAAAAGTCTGC 674

QY      293 Glu-----GlyPhe-AspPhePhePheSe 300
      |||  |||  |||  |||  |||  |||  |||  |||
DB      675 CCTTCAACACAGCATCTGTATGATCACTCTCATTTGTGGGTTCGGATTTC----- 726

QY      300 rLeuSerAsnLysValLysAspGlyThrPro---CysSerGluAspSerArgAsnValCys 319
      |||  |||  |||  |||  |||  |||  |||  |||  |||
DB      727 -----ACAAGAGTGGCAAACTGTGTGGCTGAATGACACATCCACTGTGTTTC 773

QY      319 sIleAspGlyIleCysGluLeuSerValValSerThrSerAlaHisMetProGlnProPr 339
      |||  |||  |||  |||  |||  |||  |||  |||  |||
DB      774 TTAT-----TCACTACCAATTAAACAACACACATATCCACAC----- 810

QY      339 oLysGluAspLeuPheIleLeuProAspGluTyrLysSerCysLeuArgHisLysArgSe 359
      |||  |||  |||  |||  |||  |||  |||  |||  |||
DB      811 -----AGACAGAAAGAGATC 824

QY      359 rLeuLeuArgSerHisArgAsnGluGluLeuAsnValGluThrLeuValValAspLys 379
      |||  |||  |||  |||  |||  |||  |||  |||  |||
DB      825 AGTG-----AGCATTGAACGGTTGTGTGAGACATGTGTAGTGGCAGACAA 869
```

```
QY      379 sLysMetMetGlnAsnHisGlyHisGluAsnIleThrThrTyrValLeuThrIleLeuAs 399
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB      870 AATGATGTGGGCTACCATGGCGCCAAAGACATTTGAACATTAATTGAGTGTGATGAA 929

QY      399 mMetValSerAla-----LeuPheLysAspGlyLeuMetGly----- 411
      |||  |||  |||  |||  |||  |||  |||  |||  |||
DB      930 TATTGTGAG-GTTGCCAAACTTTACCGGTGATTTCCAGCTTAGGAAACGTTGTAATATTAT 988

QY      411 ----- 411

DB      989 AGTGCCCGCTTAATTGTTCTCACAAGAGATCAGCCAACTTGGAGATAAACCATGTC 1048

QY      412 -----LysAs 413

DB      1049 AGACAAGTCCCTCGATAGCTTCTGTAAATGGCAGAAATCCATTCTCTCCCAACAAAGTGA 1108

QY      413 pGly-----ThrArgHisAspHisAlaIleLeuLeuThrG1 425
      |||  |||  |||  |||  |||  |||  |||  |||  |||
DB      1109 TGAACAACACCATTCAGAAAATGGGATTTGCCACACGATTAATGCAGTTCTTAATTACTAG 1168

QY      425 yLeuAspIleCysSerTrpLysAsnGluProCysAspThrLeuGlyPheAlaProIleSe 445
      |||  |||  |||  |||  |||  |||  |||  |||  |||
DB      1169 ATATGATATCTGCACCTTATTAATAAATAGCCCTGTGGAACACATGGGGCTGTGTGGC 1228

QY      445 rGlyMetCysSerLysTyrArgSerCysThrIleAsnGluAspThrGlyLeuAl 465
      |||  |||  |||  |||  |||  |||  |||  |||  |||
DB      1229 TGAATGTGTGACCTTGAAAGAGCTGCAGACATTAATGAAGACATTTGGCGGTTCAGC 1288

QY      465 aPheThrIleAlaHisGluSerGlyHisAsnPheGlyMetIleHisAspGlyGluGlyAs 485
      |||  |||  |||  |||  |||  |||  |||  |||  |||
DB      1289 TTTTACCATTTGCATGAGATTTGTGCACAAATTTGGTATGAACCATGATGGAATTGAAA 1348

QY      485 mMetCys-----LysLysSerGlu--GlyAsnIleMetSerProThrLeuAlaGlyAr 502
      |||  |||  |||  |||  |||  |||  |||  |||
DB      1349 TTCTTGTGGACGAAGGTCATGAAGCAGCAAACTTATGGCAGCTCACATTACTCGGAA 1408

QY      502 gAsnGlyValPheSerTrpSerProCysSerArgGlnTyrLeuHisLysPheLeuSer-- 521
      |||  |||  |||  |||  |||  |||  |||  |||
DB      1409 TACCAATCCTTTTCTGTGTGCTGTGACGTGAGACTACATCACAGCTTCTAGAATT 1468

QY      521 ----- 521

DB      1469 TCTTAACTCGGTGATTCATAAAGTGTTCATGAATCGCCAGAAAGCGTCTGATTAA 1528

QY      521 ----- 521

DB      1529 TAATAAGAACCATTTCCGTTAAATGAGCGTGTATGCGACCTTCTGATGTTTCCGG 1588

QY      522 -----ThrAlaGlnAlaIleCysLeuAla--AspGlnProLysProValLysGlu 537
      |||  |||  |||  |||  |||  |||  |||  |||
DB      1589 CGACGGCTTTGCAAGTTCAGGGCGGTGACTTGCCTTGATATGAGCCTCCCAAGCGTGAC 1648

QY      538 TyrLysTyrProGluLysLeuProGlyGluLeuTyrAspAlaAsnThrGlnCysLysTrp 557
      |||  |||  |||  |||  |||  |||  |||  |||
DB      1649 TTCTTTATCCAGCTGTGGCCCAAGTCAAGTGTATGATGTCATGAGCAATGTCTGTTTC 1708

QY      558 GlnPheGlyGluLysAlaLysLeuCys----- 566
      |||  |||  |||  |||  |||  |||  |||
DB      1709 CAGTATGAGCAACTCCCGCAATGTAAATATGGGGTCTTAGATAATAACTCTTTCAA 1768

QY      567 -MetLeuAspPheLysLys----- 572

DB      1769 CCAACTGCCAATCAGAAAATTTCTACTCCATCTATGACCTGGAACCTCCCAACCTTAA 1828

QY      573 -----Asp11 574

DB      1829 AATGTATAAACCAAGCTGTAGCCTGACCACCTTGGGCATATGTTCTTAGGATCTCAAGT 1888

QY      574 eCysLysAlaLeuTyrCysHisArgIleGlyArgLysCysGluThrLysPheMetProAl 594
      |||  |||  |||  |||  |||  |||  |||  |||
DB      1889 GTGTAGAGAGCTCTGTGTCTCAGCAAAAGCAACCGCTGTGTCAACCAACAGTATTTCCAGC 1948
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QY 594 aAlaGluGlyThrIleCysGly-----HisAspMetTrpCysArgGlyGly 610
Db 1949 AGCTGAGGGGACACTGTGTCAAACTGGGAATATTGAAAAAGGGTGTGTATCAGGGAGA 2008
QY 610 nCysValLysTyrGlyAspGluGlyProLysProThrHisGlyHisIleTyrSerAspTyrSe 630
Db 2009 TTGTGTTCCTTTGGC--ACTTGGCCCCAGAGCATGATGGGGGCTGGGGCTTGGTC 2065
QY 630 rSerTyrSerProCysSerArgThrCysGlyGlyValSerHisArgSerArgLeuCy 650
Db 2066 ACTATGGGGAGAGTCAGACAGACCTCGGGGGAGCGCTCTTCATCCCTTAAGACACTG 2125
QY 650 sThrAsnPro-----LysProSerHisGlyGlyLysPheCysGluGlySe 665
Db 2126 TGACAGTCCAGACGCTAAGTACCTTAACACAGATCCATGCCCTTGGGTTCCCGAGATTTCG 2185
QY 665 rThrArgThrLeuLysLeuCysAsnSerGlnLysCysProArgAspSerValAspPheAr 685
Db 2186 AAGGAAACGGTATCGCTCCCTGTAAACACAGATCCATGCCCTTGGGTTCCCGAGATTTCG 2245
QY 685 gAlaAlaGlnCysAlaGluHisAsnSerArgArgPheArgGlyArgHisTyrLysTyrLly 705
Db 2246 AGAGAAACAGTGTGCAGACTTTGACAATATAGCTTTCCGAGAAAGTATTATTAACCTGAA 2305
QY 705 sProTyrThrGlnValGluAspGlnAspLeuCysLysLeuTyrCysIleAlaGluGlyPh 725
Db 2306 ACCCTATACTGAGGTGGGGTAAACCT--TGTCATTAACTGCTTGGCTGAAGGTTA 2362
QY 725 eAspPhePheSerLeuSerAsnLysValLysAspGlyThrProCysSerGluAspSe 745
Db 2363 TAATTCTACACTGAACGTCGCTCGGTGATGATGGAGCCAGTGCATGCGGATTTC 2422
QY 745 rArgAsnValCysIleAspGlyIleCysGluArgValGlyCysAspAsnValleuGlySe 765
Db 2423 ACTGATATCTGCATCAATGAGATGCAAGCACTAGGCTGTGATATATTTGGATC 2482
QY 765 rAspAlaValGluAspValCysGlyValCysAsnGlyAsnAsnSerAlaCysThrIleHi 785
Db 2483 TGATGCTAGGGAAGATAGATGTGAGTCTGTGAGGGGACGGAAGCACATGTGATGCCAT 2542
QY 785 sArgGlyLeuTyrThrLysHisHisIleThrAsnGlnTyrTyrHisMetValThrIlePr 805
Db 2543 TGAAGGTTCTTCAATGATTCATGCCAGGGGAGGCTACATGGAAGTGTGCAGATACC 2602
QY 805 oSerGlyAlaArgSerIleArgIleTyrGluMetAsnValSerThrSerTyrIleSerVa 825
Db 2603 AAGAGGCTCTGTTCACATGTGAAGTTAGAGAAGTGCATGTCAAGAAGACTATTTGCTTT 2662
QY 825 lArgAsnAlaLeuArgArgTyrTyrLeuAsnGlyHisIleThrValAspTyrProGlyAr 845
Db 2663 AAAATCTGAAGAGATGATTAATATATTAAAGTGTGCCTGACTATTGACCTAGGAA 2722
QY 845 gTyrLysPheSerGlyThrThrPheAspTyrArgArgSerTyrAsnGluProGluAsnLe 865
Db 2723 ATTTGATGTGTCTGGACAGCTTTTCATTACAGAGACCAACTGATGAACCAAGATCCTT 2782
QY 865 uIleAlaThrGlyProThrAsnGluThrLeuIleValGluLeuLeuPheGlnGlyArgAs 885
Db 2783 GGAAGCTCTAGGTCCTACCTCAGAAATCATCTCATGGTCTTCTGCTTCAAGAACAGAA 2842
QY 885 nProGlyValAlaTyrGluTyrSerMetPro-----ArgLeuGlyThrGluLysGlnPr 903
Db 2843 TTTGGAAATAGTATTAAGTTCAATGTTCATTCACATCACTGAACTGGCAGTGGAGATAAT-- 2900
QY 903 oProAlaGlnProSerTyrThrTyrPalaIleValArg---SerGluCysSerValSerCy 922
Db 2901 -----GAAGTTGGCTTTACATGGAATCATCAGCCTTGGTCAGAATGCTCAGCTACTTG 2953
QY 922 sGlyGlyArg 926
Db 2954 TGCTGAGGTTAAG 2966

RESULT 10

US-09-799-451-411
; Sequence 411, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969e1 Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pc_fl_genes Version 2.0
; SEQ ID NO 411
; LENGTH: 3571
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (260)..(3568)
US-09-799-451-411

Alignment Scores:
Pred. No.: 2.09e-105 Length: 3571
Score: 1247.50 Matches: 320
Percent Similarity: 44.58% Conservative: 141
Best Local Similarity: 30.95% Mismatches: 343
Query Match: 23.83% Indels: 233
DB: 4 Gaps: 27

US-09-981-151D-8 (1-952) x US-09-799-451-411 (1-3571)
QY 19 AlaglnValAlaGluGlnValSerProGlyArg----- 29
Db 6 TCCCGGTGACGATTTCTAGGCCCGCGGCGCAGGCTCCAAGAAGAAACC 65
QY 30 SerHisGlnArg-GlyAsnArgGlySerGlyGlnLeuGluAlaSerProProArgLeuLe 49
Db 66 AAGGCCAGAGAGGAGGCCACAGTGCAGGAGCAGGCGAAGGATCCG----- 117
QY 49 uSerArgGlyProArgArgLeu-ThrAlaMetSerProLeuPheSerAlaGlyThrCysV 69
Db 118 -TACAGGGGCCCAACACTACTCAACCAACGAAGCCCCCAAAGAGCCCGGTGATGCTG 176
QY 69 aLArgHisGlyThrArgSerGlySerAlaTyrGluProGluArgProAlaSerSerSert 89
Db 177 CGAAGGCTGTAACAGGGGAGGC-----GGCA 203
QY 89 hrArgGlyAlaAlaGlyLeuAspGlyLysGlyArgAspMet----- 102
Db 204 CTGTGGGGGCTGCCGGCAG-CCGGGGTGGGAGAGACATGTGACACGTGGCCTGTATG 262
QY 103 -----AspGluAlaGlyAsnHis--ArgS 110
Db 263 GCTCCGCCCTGCCAGATCCTCCGCTGGGCCCTCGCCCTGGGGCTGATGTTCAG 322
QY 110 erGlnGlnThrAsnThrGlyThrGluAsnGlnThrLeuHisValLeuThrGlnTyrAspL 130

DB 323 G-TCAAGCACGCGCTTCCGGTCT-CAAGATGAGTTCTGTCCAGTCTGGAGAGACTATGAGA 380
QY 130 euValSerAlaTyrGluValAspHisArgGlyAspTyrValSerHisGluIleMetHisH 150
DB 381 TGGCCTTCCCCACCGCGCTGGACCAACAAGGGGCACTGCTGGCCTTCTCGCCACCTCCTC 440
QY 150 IsGlnArgArgArgAlaValAlaValSerGluValGluSerLeuHisLeuArgLeuL 170
DB 441 CCCGAGGACGCGCGCGGACAGGGGGGCCACAGCCGAGTCCCGCCTTCTTACAAGTAG 500
QY 170 ySgLYProArgHisAspPheHisMetAspLeuArgThrSerSerSerLeuValAlaProG 190
DB 501 CTTGGGCCAGCACCCCACTTCTGTGTAACCTGACCCGAGCTCCCGTCTACTGGCAGGGC 560
QY 190 lYpHeIleValGlnThrLeuGlyLysThrGlyThrLysSerValGlnThrLeuProG 210
DB 561 ACGTCTCCGTGGAGTACTGGACACGGGAGGGCCTGGCCTGGCAGAGGGCGGGCCGCC 620
QY 210 lUAspPheCySPheTYrGlnGlySerLeuArgSerHisArgAsnSer----- 225
DB 621 AC-----TGCTCTACGCTGTGTCACTTCAGGGGCCAGGCCAGCACTCCCATGTGGCCA 674
QY 225 ----- 225
DB 675 TCAGCACCTGTGAGGCGCTGCACGCGCTGATCGTGGCAGACGAGAAGTAGTACTGATTG 734
QY 226 --ProSerHisGlyGlyLysPheCySGlySerThrArgThrLeuLysLeuCyAsnS 245
DB 735 AGCCCTGCACGGTGGGCC-----AAGGTTCT----- 763
QY 245 eRglnLysCySProArgAspSer-----ValAspPheArgAlaAlaGln----- 259
DB 764 -----CGAGCGCGGAGGAAGAAGTGGACCAACATGTGGTGTACAGCGTTCCTGTGCGTC 818
QY 260 -----CysAlaGlnHisAsnSerArgArgPheArgGlyArgHisT 273
DB 819 ACCCCCACTGGACACAGCCTGTGGAGTGAAGATGAGAACCGTGGAAAGGGCGGCAT 878
QY 273 yTLySTrPlySProTYrThrGlnValGluAlaAspLeuCySlyLeuTYrCysIleAlaG 293
DB 879 GGTGGCTGCGGACCTTGAAGSCACCGCCTGCCAGA----- 913
QY 293 lUcLYPheAspPhePheSerLeuSerAsnLysValLysAspGlyThrProCysSerG 313
DB 914 -----CCCTGGGGAATGAACAAGAGCGTGGCCAGCCA----- 946
QY 313 lUAspSerArgAsnValCysIleAspGlyIleCySgLUleuSerValValSerThrSera 333
DB 947 -----GGCCTG----- 952
QY 333 lAhISMetProGlnProProLysGluAspLeuPheIleLeuProAspGlyTYrLysSerc 353
DB 952 ----- 952
QY 353 ySLeuArgHisLysArgSerLeuLeuArgSerHisArgAsnGluGluLysAsnValGluT 373
DB 953 -----AAGCGATCGGTCAAGCCGA-----GAGCGCTACGTGAGA 986
QY 373 hrlEuValValValAspLysLysMetMetGlnAsnHisGlyHisGluAsnIleThrThrT 393
DB 987 CCTGTGTGTGGCTGACAAGATGATGTGGCTATCAAGGGCGCGGATGTGGAGCAGT 1046
QY 393 yValLeuThrIleLeuAsnMetValSerAlaLeuPheLysAspGlyLysMetGly---- 411
DB 1047 ATGTCTGTGGCCATCATGAACATGTGTGCCAAACTTTTCCAGGACTCGAGTGTGGGAAGCA 1106
QY 411 ----- 411
DB 1107 CCGTTAACATCCTCTGTAACCTCGCCTCATCTGTCTCAGGAGACCAAGCCACCTGTGGAGA 1166
QY 411 ----- 411

DB 1167 TCACCCACCATGCGCGGAAGTCCCTAGACAGCTTCTGTAAGTGGCAGAAATCCATCGTGA 1226
QY 412 -----LysAspGly---ThrArgHisAspHisAlaI 421
DB 1227 ACCACAGCGGCATGGAATGGCATTCAGAGAAACGGTGTGGCTAACCATGACACAGCAG 1286
QY 421 lELeuLeuThrGlyLeuAspIleCysSerTrpLysAsnGluProCysAspTrpLeuGlyP 441
DB 1287 TGCTCATCACAGCTATGACATCTGCATCTACAAAGAACAAACCTTGGCGCACACTAGGCC 1346
QY 441 heAlaProIleSerGlyMetCysSerLysTYrArgSerCysThrIleAsnGluAspThrG 461
DB 1347 TGGCCCGCGGTGGCGGAATGTGTGAGCGCGAGAGAAGCTGCAGCGCTCAATGAGACATTG 1406
QY 461 lYLeuGlyLeuAlaPheThrIleAlaHisGluSerGlyHisAsnPheGlyMetIleHisA 481
DB 1407 GCCTGCCACAGCGCTTACCACTTGGCCACGAGATCGGCACACATTCGGCATGAACCATG 1466
QY 481 sPGLyGlyLysMetCys-----LysLysSerGlyLysAsnIleMetSerProt 498
DB 1467 ACGCGGTGGGAACAAGCTGTGGGGCCCGGTGTCAAGGACCCAGCCAAAGCTCAAGCTGCC 1526
QY 498 hrlEuAlaGlyArgAsnGlyValPheSerTrpSerProCysSerArgGlnTYrLeuHisL 518
DB 1527 ACATTACCATGAAGAACCAACCACTTCGTGTGTCTCATCTGCACACCGTACTATCATCACA 1586
QY 518 ySPheLeuSerThrAlaGlnAlaIleCysLeuAlaAspGlnProLysProValLysGluT 538
DB 1587 GCTTTTACACTCGGGCGCTGGGGCTGTCTCTGAACAACCGGCC--CCACAGACAGACT 1643
QY 538 yTLySTyrProGluLysLeuProGlyGlyLeuTYrAspAlaAsnThrGlnCySlySTrG 558
DB 1644 TTGTGTACCCGACAGTGGCACCGGGCCCAAGCCTTACGATGCAGATGAGCAATGCCCTTTC 1703
QY 558 lnpHeGlyGlyLysAlaLysLeuCySMetLeuAspPheLysAspIleCySlyAlaL 578
DB 1704 AGCATGGAAGTAAATCGCGCTGATGTAAATACGGG-----GAGGTCTGCAGCGAGC 1754
QY 578 euTrpCysHisArgIleGlyArgLysCysGluThrLysPheMetProAlaAlaGlyLUT 598
DB 1755 TGTGTGTCTGAGCAAGACCAACCGGTGCATCAACAACAGCATCCCGCGCGCGAGGGCA 1814
QY 598 hrlLeCys---GlyHisAspMet-----TrpCysArgGlyGlyGlnCysValLysT 614
DB 1815 CGCTGTGCCAGACGACACCACTGCACAAGGGGTGTGTCTACAACGGGTGTGTTCCT 1874
QY 614 yTGlyAspGlyLysProLysProThrHisGlyHisTTrpSerAspTrpSerSerTrpSerp 634
DB 1875 TTGGGTGGCGC--CCAGAGGGTGTGACAGGACCTGGGGCGGTGACTCATATGGGGCG 1931
QY 634 roCysSerArgThrCysGlyGlyGlyValSerHisArgSerArgLeuCysThrAsnProL 654
DB 1932 ACTGCAGCGGACCTGTGGCGGGCGGTGTCTTCTTAGTGTCACTGCACAGCCCCCA 1991
QY 654 ySProSerHisGlyGlyLysPheCysGlyLysSerThrArgThrLeuLysLeuCyAsnS 674
DB 1992 GGGCAACCATCGGGGCAAGTACTGTGTGGGTGAAGAGCGGCACCGCTCTCCCAACA 2051
QY 674 eRglnLysCySProArgAspSerValAspPheArgAlaAlaGlnCysAlaGlnHisAsnS 694
DB 2052 CGGATGACTGTCCCGCTGCTCCAGACTTCAGAGAAAGTGCAGTGTCTGAATTGGACA 2111
QY 694 eRArgArgPheArgGlyArgHisTTrpLysTrpLysProTYrThrGlnValGluAspGlnA 714
DB 2112 GCATCCCTTTCCTGGGAAATTTCTACAAGTGAAGAAACGTAC--CGGAGAGGGCGGTGA 2168
QY 714 sPLeuCySlyLeuTYrCysIleAlaGluGlyPheAspPhePheSerLeuSerAsnL 734
DB 2169 AGCCTGTGCTCCTCACGTGCTTAGCGGAAGCTTCAACTTCTACACGAGAGGGCGGCAG 2228
QY 734 ySValLysAspGlyThrProCysSerGlyAspSerArgAsnValCysIleAspGlyIleC 754
DB 2229 CCGTGTGAGCGGACACCCCTGCGTCCAGACACGGTGAACATTTGCGTCAGTGGCGAAT 2288

[illegible]

```

RESULT 11
US-09-392-184-5/c
; Sequence 5, Application US/09392184
; Patent No. 6395889
; GENERAL INFORMATION:
; APPLICANT: Robison, Kelth E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: PROTEASE HOMOLOGS
; FILE REFERENCE: 5800-55
; CURRENT APPLICATION NUMBER: US/09/392,184
; CURRENT FILING DATE: 1999-09-09
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for windows Version 3.0
; SEQ ID NO 5
; LENGTH: 5357
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(5357)
; OTHER INFORMATION: reprotolysin (ADAM family of metalloprotease)
; NAME/KEY: misc_feature
; LOCATION: (1)..(5357)
; OTHER INFORMATION: n = A,T,C or G
US-09-392-184-5

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Alignment Scores:	
Pred. No.:	6.36e-105
Score:	1245.50
Percent Similarity:	48.78%
Best Local Similarity:	33.58%
Query Match:	23.79%
DB:	3
	Length: 5357
	Matches: 316
	Conservative: 143
	Mismatches: 329
	Indels: 153
	Gaps: 32

US-09-981-151D-8 (1-952) x US-09-392-184-5 (1-5357)

402 SerAlaLeuPheLysAspGlyLeuMetGlyLys-----412

Qy	53	ProArgArgLeuThrAlaMetSerProLeuPheSerAlaGlyThrCysValArgHisGly	72
Db	5357	CCNAAGGGAATTAAGCTTGGCGCGCC-----GGTTCCTGC-----CATGCC	5316
Qy	73	ThrArgSerGlySerAlaTrpGluProGluArgProAlaSerSerSerThrArgGlyAla	92
Db	5315	CGCGCGCCCAAGTCC-----CCGAGCCCCCGGCTTGTGCTGCGCCCCCTCTCT	5265
Qy	93	AlaGlyLeuAspGlyLysGlyArgAspMetAspGluAlaGlyAsnHisArgSerGln---	111
Db	5264	GCTCTCTCTG-----CGTCTGGCTCCCGCGCGCCCCCGGACC	5229
Qy	112	GlnThrAsnThr-GlyThrGluAsnGlnThrLeuHisValLeuThrGlnTyrrAspLeuVal	131
Db	5228	CGCACCAGGACGTGCACACCGAGGCGCG-----GCCGCACTGCACATCGT	5184
Qy	131	IserAlaTyrrGluValAspHisArgGlyAspTyrrValSerHisGlyIleMetHisGly	151
Db	5183	GCACCCGGTTTCAGTCGACGCGCGGGGCTCTCTCTCTCTCTACGAGCTGTGCCCCCGCC	5124
Qy	151	narGArgArgAlaValAlaValAspGluValGluSerLeuHisIleuArgLeuLysGly	171
Db	5123	ACTGCGCAGCGGGATGATATCTGTGCGCCGAGACGCGCGCCCTTTCAGAGCTACAAATA	5064
Qy	171	yrProArgHisAspPheHisMetAspLeuArgThrSerSerSer-LeuValAlaProGlyP	191
Db	5063	CCGCGGGCGGAGCTGCGCTTCACCTGACCGCCAAATCAAGCACCTGTGGCGCGCGCT	5004
Qy	191	heIleValGlnThrLeuGlyLysThrGlyThrLysSerValGlnThrLeuProProGluA	211
Db	5003	TTGTGAGCGAGACGCGCGGCGCGCGCTGGCGCGCGCACATCGGGGCCACACCC	4944
Qy	211	srPheCysPheTyrrGlnGlySerLeuArgSerHisArgAsnSerProSerHisGlyGly-	230
Db	4943	CGGCCTGCCACCTGCTTGGCGAGGTG-----CAGGACCTGAGCTCGAGGGTGGCC	4893
Qy	231	-----LysPheCysGluGlySerThrArgThrLeuLysLeuCysAsnSerGlnL	247
Db	4892	TGGCGGCATCAGCGCTCGCGACGCGCTGAAGAAGTGTGTTCAGACTCTCCAAAGAGACT	4833
Qy	247	ysCys-----ProArgAspSerValAspPheArgAlaAlaGlnCysAlaGlnHis----	263
Db	4832	ACTTCATTGAGCCCCCTGACAGTAGTCCCCCGCGCGCTGGCCACGCCCCCATGTGG	4773
Qy	264	-----AsnSerArgArgPheArgGlyArgHisTyrrLysTrpLysProTyrrThrGlnVal	281
Db	4772	TGTACAAGCGTCAGGCCCCCGAGAGGCTGGCACAGCGGGGTGATTCCAGTCTCCAAAGCA	4713
Qy	282	GluAlaAspLeuCysLysLeuTyrrCysIleAlaGlnGlyPheAspPhePheSerLeu	301
Db	4712	CCTGTGAG--TGCAAG-----	4698
Qy	302	SerAsnLysValLysAspGlyThrProCysSerGlnAspSerArgAsnValCysIleAsp	321
Db	4697	-----TGTACCCAG-----ACGTGAGTCTGCAC	4674
Qy	322	GlyTyrCysGluLeuSerValIleSerThrSerAlaHisMetProGlnProProLysGlu	341
Db	4673	GGG-----AGCGTTGGAGACGCGGACGAGTGGCGCGGCGCCACGGCTGAGG	4626
Qy	342	AspLeuPheIleLeuProAspGlyTyrrLysSerCysLeuArgHisLysArgSerLeuLeu	361
Db	4625	CGTCTA-----CACACGCGGTGGTC--	4605
Qy	362	ArgSerHisArgAsnGluGluLeuAsnValGlnThrLeuValValAspLysLysMet	381
Db	4604	-----AGCAAGAGAGTGGGTGGAGACCTGTAGTACGTGATGCCAAATG	4557
Qy	382	MetGlnAsnHisGlyHisGluAsnIleThrThrTyrrValLeuThrIleLeuAsnMetVal	401
Db	4556	GTGAGTACACGACGACCGCGCAGGTGAGAGTATGTGCTGACCAATCATGAACATGGTG	4497
Qy	402	SerAlaLeuPheLysAspGlyLeuMetGlyLys-----	412

412

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QY 413 -----AspGlyThr--- 415
DB 4436 GTCCCTGCGAAGATGAGGAGGAGACCTAAAGATCACGACCATGACAGACAACACCCCTG 4377
QY 416 -----Arg 416
DB 4376 AAGAGCTTTCGAGTGGCAGAAAACATCAACATGAAGGGGATGCCCATCCCTGCAC 4317
QY 417 HisAPHisAlaIleLeuLeuThrglyLeuAspIleCysSerTrpLysAsnGluProCys 436
DB 4316 CATGACACCTGCTCCTGCTCAGCAAGAACGACCTGTGTGACAGCATGAACCGGCTGT 4257
QY 437 AspThrLeuGlyPheAlaProIleSerGlyMetCysSerLysTrpArgSerCysThrIle 456
DB 4256 GAGACCTGGAGCTGTCCCATGTGGCGGGCATGTGCCAGCCGACCGCAGCTGCAGCATC 4197
QY 457 AsnGluAspThrGlyLeuGlyLeuAlaPheThrIleAlaHisGluSerGlyHisAsnPhe 476
DB 4196 AACGAGACACGGGCTGCGCGCTGCGCTTCACTGTAGCCACGAGCTCGGGCAGATT 4137
QY 477 GlyMetIleHisAspGlyGluGlyAsnMetCysLysLys-----SerGluGlyAsnIle 494
DB 4136 GGCATTGACATGACGGAAGCGGCAATGACTGTGAGCCCGTTGGGAAACGACCTTTCATC 4077
QY 495 MetSerProThrLeuAlaGlyArgAsnGlyValPheSerTrpSerProCysSerArgGln 514
DB 4076 ATGTCTCCACAGCTCCTGTACGACGCGCTCCCTCACCTGTGCTCCGCTGCAGCGCCAG 4017
QY 515 TyrLeuHisLysPheLeuSerThrAlaGlnAlaIleCysLeuAlaAspGlnPro--Lys 533
DB 4016 TATATCACCAGGTTCTTGAACGCGGGGTGGGCTGTGCTGTGACGACCTCTGCCAAG 3957
QY 534 ProValLysGluTyrLysTrpProGluLysLeuProGlyGluLeuTyrAspAlaAsnThr 553
DB 3956 GACATTATGAC-----TTCCTCGGTGCCACCTGGCGTCTCTATGATGTAAGCCAC 3903
QY 554 GlnCysLysTrpGlnPheGlyGluLysAlaLysLeuCysMetLeuAspPheLysLysAsp 573
DB 3902 CAGTGCCGCTCCAGTACGCGGCGCTACTCTGCTTCTGC-----GAGGACATGATATAT 3849
QY 574 IleCysLysAlaLeuTrpCysHisArgIleGlyArgLysCysGluThrLys--PheMetPr 593
DB 3848 GTCTGCCACACACTCTGTGTC--TCTGTGGGACACACTGTCACTCCAAGCTGGATGCA 3792
QY 593 AlaAlaGluGlyThrIleCysGlyHisAspMetTrpCysArgGlyGlyGlnCysValLys 613
DB 3791 GCCCGTGACGGGACCCGCTGTGGGGAAGATAGTGTGTCTCAGTGGGAGTCCGTACC 3732
QY 613 sTyrGlyAspGluGlyProLysProThrHisGlyHisTrpSerAspTrpSerSerTrpSe 633
DB 3731 CGTGGGCTTCCG--CCCGAGCGCTGATGTGGCTGTGCTGAGCGCTGAGCGCTGTGTC 3675
QY 633 rProCysSerArgThrCysGlyGlyGlyValSerHisArgSerArgLeuCysThrAsnPr 653
DB 3674 CATCTGCTACGAGAGCTGTGGCATGGGCGTACAGAGCGCGGAGCGCAGTGCACGACGC 3615
QY 653 OlyBProSerHisGlyGlyLysPheCysGlyGlySerThrArgThrLeuLysLeuCysAs 673
DB 3614 TACGCCCAATATCAAAAGCAGATACTGTGTGGGTGAGCGCAAGCGCTTCCGCTCTGCA 3555
QY 673 nSerGlnLysCysProArgAspSerValAspPheArgAlaAlaGlnCysAlaGluHisAs 693
DB 3554 CTTGCAGGCGCTGCTGCTGCGCGCTCTCTCCGACAGTGCAGCCACTTTGA 3495
QY 693 nSerArgArgPheArgGlyArgHisTyrLysTrpLysProTyrThrGlnValGluAspG 713
DB 3494 CGCTATGCTGTACAGGGCGCAGCTGCACACATGGGTGCCGTG-----GTCAATGACGT 3441
QY 713 nAspLeuCysLysLeuTyrCysIleAlaGluGlyPheAspPhePheSerLeuSerAs 733

DB 3440 GAACCCCTGCGAGCTGCACCTGCCGCGCCCGCAATGAGTACTTTGCCGAGAGCTGCGGGA 3381
QY 733 nLysValLysAspGlyThrProCysSerGlu-----AspSerArgAsnValCysIleAs 751
DB 3380 CGCCGTGTGATGGCACCCCTGCTACTACAGGTCCGAGCAGCCGCGGACCTGTGCATCAA 3321
QY 751 pGlyIleCysGluArgValGlyCysAspAsnValLeuGlySerAspAlaValGluAspVa 771
DB 3320 CGGCATCTGTAGAAGACGTGGGTGTGACTTGAGATTGACTCCGGTGTCTAGAGAGACCG 3261
QY 771 lCysGlyValCysAsnGlyAsnAsnSerAlaCysThrIleHisArgGlyLeuTyrThrly 791
DB 3260 CTGTGTGTGTGCCACGCGACGCGCTCCACCTGCCACACCGTGAGCGGACCTTCGAGGA 3201
QY 791 sHisHisThrAsnGlnTyrTyrHisMetValThrIleProSerGlyAlaArgSerI 811
DB 3200 GCGCGAGGCGCTGGG--TATGTGATGTGGGGCTGATCCAGCGCGCGCAGAGAT 3144
QY 811 eArgIleTyrGluMetAsnValSerThrSerTyrIleSerValArgAsnAla---LeuAr 830
DB 3143 CCGCATCCAGAGGTTGCCAGAGCTGCCAATTCTCTGCACTCGGAGTGAAGACCCGGA 3084
QY 830 gArgTyrTyrLeuAsnGlyHisTrpThrValAspTrpProGlyArgTyrLysPheSerG 850
DB 3083 GAAGTACTTCTCAATGATGTGGTGGACCATCACTGAGAACCGGGACTACCAAGTGGCAGG 3024
QY 850 yThrThrPheAspTyrArgArgSerTyrAsnGluProGluAsnLeuIleAlaThrGlyPr 870
DB 3023 GACCACCTTCACATACGACGCGAGGGGCACTGG--GAGAACCTCACGTCCTCCGGGTCC 2967
QY 870 oThrAsnGluThrLeuIleValGluLeuPheGlnGlyArgAsnProGlyValAlaTr 890
DB 2966 CACCAAGAGGCTGTCTGATCCAGCTGTCTTCCAGAGAGCAACCTGGGGTGCACTA 2907
QY 890 pGluTyrSerMetProArgLeu-----GlyThrGluLysGlnProProAlaGlnProse 908
DB 2906 CGAGTACACCATCCACAGGAGGAGGAGGTGGCCACGAGAGTCCCGCG--CCCGT 2853
QY 908 rTyrThrTrpAlaIle--ValArgSerGluCysSerValSerCysGlyGlyGly 925
DB 2852 GTTCTCTGGCATTATGGGCGCTGACCAAGTGCACAGTCACTGCGGCGAGAGGT 2798

RESULT 12
US-09-981-953A-3
; Sequence 3, Application US/09981953A
; Patent No. 6689599
; GENERAL INFORMATION:
; APPLICANT: RACIE, LISA A.
; APPLICANT: TWINE, NATALIE C.
; APPLICANT: AGOSTINO, MICHAEL J.
; APPLICANT: WOLFMAN, NEIL
; APPLICANT: MORRIS, ELISABETH A.
; TITLE OF INVENTION: NOVEL AGGRECANASE MOLECULES
; FILE REFERENCE: 08702.0075-00000
; CURRENT APPLICATION NUMBER: US/09/981,953A
; PRIOR FILING DATE: 2001-10-18
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3377
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Nucleotide
; OTHER INFORMATION: sequence of the aggrecanase molecule
US-09-981-953A-3

Alignment Scores:
Pred. No.: 5e-105 Length: 3377
Score: 1243.00 Matches: 295
Percent Similarity: 45.58% Conservative: 133

Best Local Similarity: 31.42% Mismatches: 317
Query Match: 23.74% Indels: 194
DB: 4 Gaps: 24
US-09-981-151D-8 (1-952) x US-09-981-953A-3 (1-3377)
QY 84 ProAlaSerSerSerThrArgGlyAlaAlaGlyLeuAspGlyLysGlyArgAspMetAsp 103
DB 18 CCCGCCCTGCAGATCCTCCGCTGGGCCCTGCCCTG---GGGCTGGGCTCATGTTCCAG 74
QY 104 GluAlaGlyAsnHisArgSerGlnGlnThrAsnThrGlyThrGluAsnGlnThrLeuHis 123
DB 75 GTCACGACGCGCTTCCGGTCTCAA-----GATGAGTTCTGTCC 113
QY 124 ValLeuThrGlnTyArgLeuValSerAlaTyGluValAspHisArgGlyAspTyVal 143
DB 114 AGTCTGAGAGCTATGAGATGCGCTTCCCAACCGCGGTGACCAACGGGCACTGCTG 173
QY 144 SerHisGluIleMetHisHisGlnArgArgArgAlaValAlaValSerGluValGlu 163
DB 174 GCGTTCTGCGCACTCTCCCGGAGGACGCGCGGACGGGGGCCACAGCCGAGTCC 233
QY 164 SerLeuHisLeuArgLeuLysGlyProArgHisAspPheHisMetAspLeuArgThrSer 183
DB 234 CGCCTCTTTCACAAAGTGCGCTCGCCACGACCCACTTCTGCTGAACCTGACCCGACG 293
QY 184 SerSerLeuValAlaProGlyPheIleValGlnThrLeuGlyLysThrGlyThrLysSer 203
DB 294 TCCCGTCTACTGGCAGGACGCGCTCTCCGTGAGTACTGACACGAGGCGCTGCGCTGG 353
QY 204 ValGlnThrLeuProProGluAspPheCysPheTyArgGlnGlySerLeuArgSerHisArg 223
DB 354 CAGAGACGCGCGCGCCAC-----TGCTCTACGCTGTCACTGACGGGCCAGGCC 407
QY 224 AsnSer----- 225
DB 408 AGCAGCTCCCATGTGCCATGCACAGACCTGTGAGGCGCTGCACGCGCTGATGTCGACAG 467
QY 226 -----ProSerHisGlyGlyLysPheCysGlyGlySerThrArg 238
DB 468 GAGAGAGATACCTGATTGAGCCCTGCACGCTGGGCC-----AAGGTTCT----- 515
QY 239 ThrLeuLysLeuCysAsnSerGlnLysCysProArgAspSer-----ValAspPhe 255
DB 516 -----CGAGCCCGGAGAAAGTGGAACACATGTGTGTAC 551
QY 256 ArgAlaAlaGln-----CysAlaGlnHisAsnSerArg 266
DB 552 AAGCGTCTCTCTGCGTACCCCACTGCACACAGCTGTGGAGTGAAGATGAGAA 611
QY 267 ArgPheArgGlyArgHisTyLeuTyLysProTyThrGlnValGluAlaAspLeuCys 286
DB 612 CCGTGAAAGGGCGGCATGCTGGCTGGACCTTGAAAGCCACCGCTGCCAGG----- 665
QY 287 LysLeuTyCysIleAlaGluGlyPheAspPhePheSerLeuSerAsnLysValLys 306
DB 666 -----CCCCTGGGAAATGAACAGAG 686
QY 307 AspGlyThrProCysSerGluAspSerArgAsnValCysIleAspGlyTleCysGluLeu 326
DB 687 CGTGCCAGCCA-----GGCTG----- 704
QY 327 SerValValSerThrSerAlaHisMetProGlnProProLysGluAspLeuPheIleLeu 346
DB 704 ----- 704
QY 347 ProAspGluTyLysSerCysLeuArgHisLysArgSerLeuLeuArgSerHisArgAsn 366
DB 705 -----AAGCATCGGTCAAGCGA----- 722
QY 367 GluGluLeuAsnValGluThrLeuValValAspLysLysMetMetGlnAsnHisGly 386
DB 723 ---GAGCGTACGTGAGACCTGTGTGTGCTGACAAAGATGATGTGTGCTATCACGGG 779

QY 387 HisGluAsnIleThrThrTyValLeuThrIleLeuAsnMetValSerAlaLeuPheLys 406
DB 780 CGCCGGATGTGGAGCATATGCTCTGGCCATCATGAACATTGTGGCAAACCTTTCCAG 839
QY 407 AspGlyLeuMetGly----- 411
DB 840 GACTCGAGTCTGGAGAGACCGTTAACATCCTCGTACTCGCCTCATCTGCTCACGGAG 899
QY 411 ----- 411
DB 900 GACCAAGCCCACTTGAGATCACCCACCATGCGGGAAGTCCCTGGACAGCTTCTGTAA 959
QY 412 -----LysAspGly--- 414
DB 960 TGGCAGAAATCCATCGTGAACACAGCGGTCAATGCAATGCCATTCCAGAGAACGCTGTG 1019
QY 415 ThrArgHisAspHisAlaIleLeuLeuThrGlyLeuAspIleCysSerThrLysAsnGlu 434
DB 1020 GCTAACCATGACACAGCAGTGTCTATACACGCTATGACATCTGCATCTTACAGAACAA 1079
QY 435 ProCysAspThrLeuGlyPheAlaProIleSerGlyMetCysSerLysTyArgSerCys 454
DB 1080 CCCTGCGGCACACTAGAGCTTGCGCCCGGTGGCGGAATGTGTGAGCGGAGAGAACTGC 1139
QY 455 ThrIleAsnGluAspThrGlyLeuGlyLeuAlaPheThrIleAlaHisGluSerGlyHis 474
DB 1140 AGCGTCAATGAGACATTGGCTGCGCCACAGCGTTCAACCATTTGCCACAGAGATCGGGC 1199
QY 475 AsnPheGlyMetIleHisAspGlyGluGlyAsnMetCys-----LysLysSerGlu 491
DB 1200 ACATTGGCATGAACCATGACGCGCGTGGGAAACAGCTGTGGGGCCCGGTGTCAGAGCCCA 1259
QY 492 GlyAsnIleMetSerProThrLeuAlaGlyArgAsnGlyValPheSerTrpSerProCys 511
DB 1260 GCCAAGCTCATGTGCTGCCCACTTACATGAAGACCAACCGTTCTGTGTGTCATCTGC 1319
QY 512 SerArgGlnTyLeuHisLysPheLeuSerThrAlaGlnAlaIleCysValAlaAspGln 531
DB 1320 AGCCGTACTACATCACAGCTTTCTAGACTCGGGCGCTGGGGCTCTGCTGAACAAACCGA 1379
QY 532 ProLysProValLysGlyTyLysTyProGluLysLeuProGlyGluLeuTyArgAla 551
DB 1380 CCC---CCACAGACAGCACTTGTGTACCCGACAGTGGCACCGGGCCAAACCTTACGATGCA 1436
QY 552 AsnThrGlnCysLysTrpGlnPheGlyGlyLysAlaLysLeuCysMetLeuAspPheLys 571
DB 1437 GATGAGCAATGCCGCTTTCAGCATGAGTCAAAATCGCTCAGTGAATAACGGG----- 1490
QY 572 LysAspIleCysLysAlaLeuTyTrpCysHisArgIleGlyArgLysCysGluThrLysPhe 591
DB 1491 ---GAGTCTGCAGCGAGCTGTGTGTCTGAGCAAGACCAACCGGTGATCACCAACAGC 1547
QY 592 MetProAlaAlaGlyGlyThrIleCys--GlyHisAspMet-----TrpCysArg 607
DB 1548 ATCCCGCGCCCGAGGGCACGCTGTGCTGCAGACGACCAACCATGCAGCAAGGGGTGTGTAC 1607
QY 608 GlyGlyGlnCysValLysTyArgLysArgGlyProLysProThrHisGlyHisTrpSer 627
DB 1608 AAACGGTCTGTGTCCCTTGGGTGGCGC--CAAGAGGTGTGACGGAGGCTGGGG 1664
QY 628 AspTrpSerSerTrpSerProCysSerArgThrCysGlyGlyGlyValSerHisArgSer 647
DB 1665 CGTGACTCCATGGGCGCACTGCAGCGGAGACCTGTGGCGGGCGGTCTTCTTAC 1724
QY 648 ArgLeuCysThrAsnProLysProSerHisGlyLysLysPheCysGluGlySerThrArg 667
DB 1725 CGTCACTGCAGACGCCCAAGCCAAACATCGGGGCAAGTACTGTGTGGGTGAGAGAGG 1784
QY 668 ThrLeuLysLeuCysAsnSerGlnLysCysProArgAspSerValAspPheArgAlaAla 687
DB 1785 CGGACCGCTCTGTGAACACGAGATGATGTCCCTGCTCCAGAGACTTCAAGAGAGTG 1844

[illegible]

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RESULT 13
US-09-981-953A-1
; Sequence 1, Application US/09981953A
; Patent No. 6689539
; GENERAL INFORMATION:
; APPLICANT: RACIE, LISA A.
; APPLICANT: TWINE, NATALIE C.
; APPLICANT: AGOSTINO, MICHAEL J.
; APPLICANT: MOLEMAN, NEIL
; APPLICANT: MORRIS, ELISABETH A.
; TITLE OF INVENTION: NOVEL AGGREGANASE MOLECULES
; FILE REFERENCE: 08702.0075-00000
; CURRENT APPLICATION NUMBER: US/09/981, 953A
; CURRENT FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/242,317
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3766
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Nucleotide
; OTHER INFORMATION: sequence of the aggreganase molecule
;

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US-09-981-953A-1	
Alignment Scores:	
Pred. No.:	2.18e-104
Score:	1237.00
Percent Similarity:	44.88%
Best Local Similarity:	31.02%
Query Match:	23.62%
DB:	4
US-09-981-151D-8 (1-952) x US-09-981-953A-1 (1-3766)	
	Length: 3766
	Matches: 318
	Conservative: 142
	Mismatches: 342
	Indels: 227
	Gaps: 27

[illegible]


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Db      842 GAGAGATGAGAAACCGTGAAGGGCGGCATGCTGGCGGACCTTGAAGCCACCGCC 901
QY      282 uAlAsrLeuCySylsLeuTyrCySIlleAgluGlYpHeAsrPhePheSerLeuSe 302
Db      902 TGCCAGG-----CCCTGGG 916
QY      302 rAsnLysValLysAsrGlYThrProCySserGluAsrSerArgAsnValCySIlleAsrGl 322
Db      917 GAATGAACAAGACGCTGGCCAGCCA-----GG 943
QY      322 YlLeCySgluLeuSerValSerThrSerAlaHisMetProGlnProProlYsGluAs 342
Db      944 CTG----- 947
QY      342 pLeuPheIlleuProAsrGlutYrLysSerCySleuArgHisLysAsrSerLeuLeuAr 362
Db      948 -----AAGCGATCGGTCAAGCCG 964
QY      362 gSerHisArgAsnGluGluLeuAsnValGluThrLeuValValAsrLysLysMetMe 382
Db      965 A-----GAGCGCTACGTGAGACCCCTGTGTGGCTGACAGAATGATGTTG 1009
QY      382 tGlnAsnHisGluHisGluAsnIlleThrThrYrValLeuThrIlleLeuAsnMetValSe 402
Db      1010 GGCCTATCACGGGCGCGCGGATGTGGAGCAGATATGTCCTGGCCATCATGAACATTGTTGC 1069
QY      402 rAlaLeuPheLysAsrGlYLeuMetGly----- 411
Db      1070 CAAACTTTCCAGGACTCGAGTCTGGGAAGCAGCCTTAACATCCTCGTACTCGCCTCAT 1129
QY      411 ----- 411
Db      1130 CCTGCTCAGGAGGACGACCCCACTGTGAGATCACCCACCATGCGGAGTCCCTGGA 1189
QY      411 ----- 411
Db      1190 CAGCTTCTGTAAGTGCAGAAATCCATCGTGAACCAAGCGGCCATGSCAATGCCATTCC 1249
QY      412 -LysAsrGlY---ThrArgHisAsrHisAlaIlleLeuLeuThrGlYLeuAsrIlleCySe 430
Db      1250 AGAGAACCGGTGGCTAACCCATGAACAGACAGTGTCTCATCACGCTATGACATCTGCAT 1309
QY      430 rTrpLysAsnGluProCySAsrThrLeuGluYpHeAlaProIlleSerGlyMetCySerLys 450
Db      1310 CTACAAGAACAAACCTGCGGCACTAGGCTGCGCCCGGTGGCGGAGATGTGTGAGCG 1369
QY      450 sTyrArgSerCySthrIlleAsnGluAsrThrGlYLeuGluYLeuAlaPheThrIlleAlaH 470
Db      1370 CGAAGAGAAGCTGCAAGCTCATAGGACATTTGACCTGGCCACAGCGTTCCACCATTTGCCCA 1429
QY      470 gLusSerGluHisAsnPheGlyMetIlleHisAsrGlYgluGluYAsnMetCyS----- 487
Db      1430 CGAGATCGGGCACAACATTCCGGCATGAACCATGACGCGGTGGGAAACAGCTGTGGGGCCG 1489
QY      488 -LysLysSerGluGluYAsnIlleMetSerProThrLeuAlaGluYArgAsnGluValPheSe 507
Db      1490 TGGTCAGGAGCCCAAGCTCATGGCTGCCCAACATTACCATGAAGACCAACCATTCGT 1549
QY      507 rTrpSerProCySserArgGlnTyrLeuHisLysPheLeuSerThrAlaGln-AlaIlleC 527
Db      1550 GTGGTCATCTGCAAGCCGTGACTACATCACAGCTTTCTAGACTCAGGGGCTGGGGCTCT 1609
QY      527 ySleuAlaAsrGlnProLysProValLysGluTyrLysTyrProGluLysLeuProGluY 547
Db      1610 GCCTGAACAAACCGGCC---CCCAAGACAGGACTTTGTGTACCCGACAGTGGGACCGGGGCC 1666
QY      547 LuLeuTyrAsrAlaAsnThrGlnCySylsTrpGlnPheGluYgluYAlaLysLeuCySm 567
Db      1667 AAGCTTACGATGCAGATGAGCAATGCCGCTTTCAAGCATGAGTCAAAATCGCGTCAGTGTA 1726
QY      567 eLLeuAsrPheLysLysAsrIlleCySylsValAlaLeuTyrCySHisArgIlleGluYArgLysC 587

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Db      1727 A-ATA-----CGGGAGGTCTGCAGCGAGCTGTGTCTGAGCAAGCAACCGGT 1776
QY      587 ySgluThrLysPheMetProAlaAlaGluGluYThrIlleCyS---GluHisAsrMet---- 604
Db      1777 GCATCACCAACAGATCCGGCGCGCGGAGGCGACGCTGTGCCAGACGACACCATCGACA 1836
QY      605 -----TrpCySArgGluYgluGlnCySValLysTyrGluYAsrGluGluYProLysProThrH 623
Db      1837 AGGGTGTGTCTACAACGGGTCTGTGTCTCCCTTGGGTGGCGC---CCAGAGGTGTGG 1893
QY      623 lSglYHisTrpSerAsrTrpSerSerTrpSerProCySserArgThrCySglYglYlv 643
Db      1894 ACGAGCTGGGGCGCGGTGAGCTTCATGGGGCGAGCTGCAGCCGAGCTGTGGCGGCGC 1953
QY      643 aLserHisArgSerArgLeuCySThrAsnProLysProSerHisGluYglYLysPheCySg 663
Db      1954 TGTCTCTTCTAGCCGCTCACTGCGACAGCCCAAGCCACATCGGGGCAAGTACTGTTC 2013
QY      663 LuGlySerThrArgThrLeuLysLeuCySAsnSerGlnLysCySProArgAsrSerValA 683
Db      2014 TGGGTGAAGAAGGCGGACCGCTCTGTCAACACAGATGACTGTCCCTGGCTCCAGG 2073
QY      683 sPHeArgAlaAlaGlnCySAlaGlnHisAsnSerArgArgPheArgGluYArgHisTyrL 703
Db      2074 ACTTCAGAAAGTGCAGTGTCTGAATTGTACAGACATCCCTTCCGTGGGAAATTTCTACA 2133
QY      703 ySTrPlyProTyrThrGlnValGluAsrGlnAsrLeuCySylsLeuTyrCySIlleAlaG 723
Db      2134 AGTGAACAAGTAC---CGGGAGGGGCGTGAAGGCTGTCTGCTACGTGCTAGCGG 2190
QY      723 LuGlyPheAsrPhePhePheSerLeuSerAsnLysValLysAsrGlYThrProCySserG 743
Db      2191 AAGCTTCAACTTTCACAGGAGGCGGACGCGCTGTGTGACGGGACACCTGCGCTC 2250
QY      743 LuAsrSerArgAsnValCySIlleAsrGlYlLeCySgluArgValGluCySAsrAsnValL 763
Db      2251 CAGACACGGTGCACATTGTGCTCAGTGGCGAATGACAGCACGTGGGTGCGACCGAGTTC 2310
QY      763 euGlySerAsrAlaValGluAsrValCySglYValCySAsnGluYAsnAsnSerAlaCySt 783
Db      2311 TGGGTCTCGACCTGCGGAGGAGCAAGTGCAGAGTGTGTGGCGGTGACGGCAGTGCCTGG 2370
QY      783 hrIlleHisArgGluYLeuTyrThrLysHisHisHisThrAsnGlnTyrTyrHisMetValT 803
Db      2371 AGACCATCGAGGCGGTCTTCAAGCCAGCTCACCTGGGGCGGGTACAGAGATGTGCTT 2430
QY      803 hrIlleProSerGluYAlaArgSerIlleArgIlleTyrGluMetAsnValSerThrSerTyrI 823
Db      2431 GGATTTCCCAAGGCTCGCTCCACATCTTCATCCAGGATCTGAACCTGTCTCAGTACT 2490
QY      823 leSerValArgAsnAlaLeuArgArgTyrTyrLeuAsnGluYHisTrpThrValAsrTrp 843
Db      2491 TGGCCTGAAGGAGGACCAAGAGTCCCTGCTGTGAGGGGCTGCCGGGACCCCCAGC 2550
QY      843 roGluYArgTyrLysPheSerGluYThrThrPheAsrTyrArgArgSerTyrAsnGluProG 863
Db      2551 CCCACGCTCTGCTCTAGCTGGAGCACCTTCACTGCGACAGGGGCCAGACCAAGTTC 2610
QY      863 LuAsnLeuIlleAlaThrGluProThrAsnGluThrLeuIlleValGluLeuLeuPheGlnG 883
Db      2611 AGAGCTCGAAGCCCTGGGAGCCGATTAATGCATCTTCATCGTCATGTGTGTCGCCGA 2670
QY      883 LuArgAsnProGluYValAlaTrpGluTyrSerMetProArgLeuGluYThrGluLysGlnP 903
Db      2671 CCGAGCTGCTGCGCTCCGCTACCGCTCAATGACCC---ATCGCCCGTGACTCGCTGC 2727
QY      903 roProAlaGlnProSerTyrThrTrpAlaIlleValArg---SerGluCySserValSerC 922
Db      2728 CCCC-----TACTCTGGAATATGCGCCCTGACCAAGTGTCTCGGCCAGT 2775
QY      922 ySglYglYglY 925
Db      2776 GTGCAAGCGGT 2786

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RESULT 14
US-09-369-364A-4
; Sequence 4, Application US/09369364A
; Patent No. 6391610
; GENERAL INFORMATION:
; APPLICANT: Apte, Suneel
; APPLICANT: Hurskainen, Tiina L.
; APPLICANT: Hirohata, Satoshi
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; FILE REFERENCE: 26473/4007/10-30-00
; CURRENT APPLICATION NUMBER: US/09/369,364A
; CURRENT FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2848
; TYPE: DNA
; ORGANISM: Homo sapiens ADAMTS-6
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (22)..(2601)
; NAME/KEY: misc feature
; LOCATION: (1369)
; OTHER INFORMATION: n = C
; NAME/KEY: misc feature
; LOCATION: (1620)
; OTHER INFORMATION: n=C
US-09-369-364A-4
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Alignment Scores:
Pred. No.:      8.01e-103      length:      2848
Score:          1218.00        Matches:      290
Percent Similarity: 45.08%      Conservative: 122
Best Local Similarity: 31.73%      Mismatches:   286
Query Match:     23.26%         Indels:       218
DB:              3             Gaps:          21
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US-09-981-151D-8 (1-952) x US-09-369-364A-4 (1-2848)

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DB      85 CATAGTGACCACAGGCTTTCATACAGTTCTCAAGAGGAATTCTGACTTATCTGAACAC 144

QY      128 TyrAspLeuValSerAlaTyrGluValAspHisArgGlyAspTyrValSerHisGluIle 147
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB      145 TACCAGCTAACTATTCCAAATAAAGGCTGATCAAAATGAGACATTTCTCAGCTTTAAGTGTG 204

QY      148 MetHis-----HisGlnArgArgArgAlaVal-----AlaValSerGlu 161
      ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
DB      205 AAAAATGATAAACACTCAAGAGAGAGACGAGATGACCCTATTGATCCACAGCAGGCA 264

QY      162 ValGluSerLeuHisLeuArgLeuGlyProArgHisAspPheHisMetAspLeuArg 181
      |||  |||  |||  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  |||
DB      265 GTATCTAAGTTATTTTAAACTTTCAAGCCTATGCGCAAGCACATTTCACTTAACTTGACT 324

QY      182 ThrSerSerSerLeuValAlaProGlyPheIleValGlnThrLeuGlyLysThrGlyThr 201
      ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
DB      325 CTCACAACAGATTTTGTGCCAAACATTTTACAGTAGAATATGCGGGGAAAGATGGA--- 381

QY      202 LysSerValGlnThrLeuProGlu-----AspPheCysPheTyr 215
      |||  |||  |||  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  |||
DB      382 -----CCCAAGTGAAACATGATTTTAAACAACATGCTCATTTAC 420

QY      216 GlnGlySerLeuArgSerHisArgAsnSerProSerHisGlyGlyLysPheCysGluGly 235
      |||  |||  |||  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  |||
DB      421 ACAAGATATTTGCAAGATCAACAGTAGTACAACTAAAGTGCTTTAAGCAACTGTGTGGG 480

QY      236 SerThrArgThrLeuLysLeuCysAsnSerGlnLysCysProArgAspSerValAspPhe 255
      ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::
DB      481 TTGCATGGTGTAT----- 495

QY      256 ArgAlaAlaGlnCysAlaGlnHisAsnSerArgArgPheArgGlyArgHisTyr----- 273
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DB      496 ---GCTACAGAGATGAAGATATTT-TATCGAACCTTTAAAGAAATACCACAGAGATTTC 551
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QY      274 -----LysTrpLysProTyrThrGlnValGluAlaAspLeuCysLys 287
      |||  |||  |||  |||  |||  |||  |||  |||  |||
DB      552 CAAGCATTTAGTTATGAAAATGGCCACC-----TCATGTTAT 590

QY      288 LeuTyrCysIleAlaGlu-----GlyPhe 295
      |||  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  |||
DB      591 TTACAAAAGTCTGCCCTTCAACAACAGACATCTGTATGATCACTCATTTGGGGTTTC 650

QY      296 AspPhePhePheSerLeuSerAsnLysValLysAsp-GlyThrProCysSerGluAspSe 315
      |||  |||  |||  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  |||
DB      651 GGATTTCAACAAGAAGTGGCAAACTTGGTGGCTGAATGACACTCCACTGTT----- 702

QY      315 rArgAsnValCysIleAspGlyIleCysGlnLeuSerValValSerThrSerAlaHisMe 335
      ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  |||
DB      703 -----CTTATTCACTACCAAAATTACAAACACACATATCCACCA 740

QY      335 tProGlnProProLysGluAspLeuPheIleLeuProAspGluTyrLysSerCysLeuAr 355
      |||  |||  |||  |||  |||  |||  |||  |||  |||
DB      741 C-----AG 743

QY      355 GHisLysArgSerLeuLeuArgSerHisArgAsnGluGluLeuAsnValGluThrLeuVa 375
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DB      744 ACAGAAGAGATCAGTG-----AGCATTGAACGGTTGTGGAGACATTGGT 788

QY      375 lValValAspLysLysMetMetGlnAsnHisGlyHisGluAsnIleThrThrTyrValLe 395
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB      789 AGTGCAGACAAATGATGTTGGCTTACCATGCGCGCAAGACATTGAACATTACATTTT 848

QY      395 uThrIleLeuAsnMetValSerAlaLeuPheLysAspGlyLeuMetGly----- 411
      ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  |||
DB      849 GAGTGTGATGATATTTGTGCCAAACTTTACCGTGATTCAGCCTAGAAACGTTGTGAA 908

QY      411 ----- 411

DB      909 TATTATAGTGCCCGCTTAATTGTTCTCAGAAAGATCAGCCAAACTTGAGATAAACCA 968

QY      411 ----- 411

DB      969 CCATGACAGACAAGTCCCTCGATAGCTTCTGTAATGCGAGAAATCCATTCTCCACCA 1028

QY      412 -LysAspGly-----ThrArgHisAspHisAlaIleLeuLe 423
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB      1029 AAGTGATGAAACACCATTCAGAAATGGGATTGCCACACGATATGACGTTCTTAT 1088

QY      423 uThrGlyLeuAspIleCysSerTrpLysAsnGluProCysAspThrLeuGlyPheAlaPr 443
      ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  |||
DB      1089 TACTAGATATGATATCTGCACCTTATAAAATAAGCCCTGTGGAACACTGGGCTTGCCCTC 1148

QY      443 oIleSerGlyMetCysSerLysTyrArgSerCysThrIleAsnGluAspThrGlyLeuG1 463
      ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  ::  |||
DB      1149 TGTGGCTGGAATGTGTGAGCCTGAAGAGAGCTGACATTAAGAAGCATGGCCCTGGG 1208

QY      463 yLeuAlaPheThrIleAlaHisGluSerGlyHisAsnPheGlyMetIleHisAspGlyG1 483
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
DB      1209 TTCAGCTTTTACCATTTGCACATGAGATTGTTCACAATTTGTGATGAACCATGATGAAT 1268

QY      483 uGlyAsnMetCys-----LysLysSerGlu-GlyAsnIleMetSerProThrLeuAlaG 501
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RESULT 15
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; Sequence 6, Application US/09369364A
; Patent No. 6391610
; GENERAL INFORMATION:
; APPLICANT: Apte, Suneel
; APPLICANT: Hurskainen, Taina L.
; APPLICANT: Hirohata, Satoshi
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; FILE REFERENCE: 26473/4007/10-30-00
; CURRENT APPLICATION NUMBER: US/09/369,364A
; CURRENT FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 3218
; TYPE: DNA
; ORGANISM: Homo sapiens ADAMTS-7
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13) . (3003)
US-09-369-364A-6

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Best Local Similarity: 31.20% Mismatches: 308
Query Match: 22.65% Indels: 222
DB: 3 Gaps: 27

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Search completed: September 10, 2005, 00:02:10
Job time : 462 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 9, 2005, 23:27:10 ; Search time 1281 Seconds
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Perfect score: 5236
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Scoring table: BLOSUM62
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Searched: 7351250 seqs, 3283620254 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	5110	97.6	2997	10	US-09-981-151A-1	Sequence 1, Appl1
3	4103.5	78.4	2433	10	US-09-981-151A-3	Sequence 3, Appl1
4	3993.5	76.3	3675	17	US-10-330-176-1	Sequence 1, Appl1
5	3993.5	76.3	3675	18	US-10-275-107-16	Sequence 16, Appl1
6	3981.5	76.0	3675	13	US-10-217-774-3	Sequence 3, Appl1
7	3981.5	76.0	3675	15	US-10-296-616-1	Sequence 3, Appl1
8	3981.5	76.0	3675	21	US-10-804-457-3	Sequence 3, Appl1
9	3981.5	76.0	4042	21	US-10-217-774-5	Sequence 5, Appl1
10	3981.5	76.0	4042	21	US-10-804-457-5	Sequence 5, Appl1
11	3720	71.0	2902	10	US-09-981-151A-5	Sequence 5, Appl1
12	3291.5	62.9	4888	17	US-10-399-645-19	Sequence 19, Appl1
13	2442	46.6	3389	18	US-10-363-937-34	Sequence 34, Appl1
14	2442	46.6	3666	16	US-10-240-545A-1	Sequence 1, Appl1
15	2440	46.6	3219	18	US-10-354-983-3	Sequence 3, Appl1
16	2440	46.6	3663	18	US-10-354-983-1	Sequence 1, Appl1
17	2415.5	46.1	3445	19	US-10-391-364-86	Sequence 86, Appl1
18	2414.5	46.1	3246	19	US-10-391-364-88	Sequence 88, Appl1
19	2371.5	45.3	3630	17	US-10-161-493-123	Sequence 123, Appl1
20	2284.5	43.6	3013	14	US-10-226-560-3	Sequence 3, Appl1
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22	2271.5	43.4	2589	14	US-10-226-560-1	Sequence 1, Appl1
23	2271.5	43.4	2589	22	US-10-990-935-1	Sequence 1, Appl1
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25	2255	43.1	3555	17	US-10-188-186-129	Sequence 129, Appl1
26	2196.5	41.9	2805	18	US-10-275-107-18	Sequence 18, Appl1
27	2073	39.6	3954	18	US-10-354-983-5	Sequence 5, Appl1
28	1678.5	32.1	1476	13	US-10-217-774-1	Sequence 1, Appl1
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30	1564.5	29.9	1986	18	US-10-354-983-7	Sequence 7, Appl1
31	1391	26.6	2879	9	US-09-788-043C-2	Sequence 2, Appl1
32	1390	26.5	2727	9	US-09-963-791-1	Sequence 1, Appl1
33	1390	26.5	2727	17	US-10-419-276-1	Sequence 1, Appl1
34	1390	26.5	2727	24	US-11-027-743-1	Sequence 1, Appl1
35	1385.5	26.5	2377	14	US-10-103-377C-1	Sequence 1, Appl1
36	1380.5	26.4	6565	18	US-10-467-042-22	Sequence 22, Appl1
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38	1377.5	26.3	2052	14	US-10-103-377C-3	Sequence 3, Appl1
39	1342	25.6	1059	17	US-10-161-493-129	Sequence 129, Appl1
40	1342	25.6	1059	17	US-10-161-493-133	Sequence 133, Appl1
41	1339	25.6	1059	17	US-10-161-493-127	Sequence 127, Appl1
42	1332	25.4	1059	17	US-10-161-493-125	Sequence 125, Appl1
43	1332	25.4	1059	17	US-10-161-493-131	Sequence 131, Appl1
44	1319	25.2	2274	9	US-09-963-791-23	Sequence 23, Appl1
45	1319	25.2	2274	17	US-10-419-276-23	Sequence 23, Appl1

ALIGNMENTS

RESULT 1
US-09-981-151A-7
; Sequence 7, Application US/09981151A
; Publication No. US20030212256A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Gerlach, Valerie
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Muriel M
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A
; APPLICANT: Stone, David J
; APPLICANT: Gunther, Erik
; APPLICANT: Ellerman, Karen
; APPLICANT: Shimkets, Richard A

/ APPLICANT: Padigaru, Muralidhara
/ APPLICANT: Guo, Xiaojia
/ APPLICANT: Paturajan, Meera
/ APPLICANT: Taupier Jr, Raymond J
/ APPLICANT: Burgess, Catherine E
/ APPLICANT: Zerhusen, Bryan D
/ APPLICANT: Ramesh
/ APPLICANT: Spytek, Kimberly A
/ APPLICANT: Gangoli, Esha A
/ APPLICANT: Fernandes, Elma R
/ APPLICANT: Gorman, Linda
/ TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
/ FILE REFERENCE: 21402-168
/ CURRENT APPLICATION NUMBER: US/09/981,151A
/ CURRENT FILING DATE: 2001-10-16
/ PRIOR APPLICATION NUMBER: 60/241,040
/ PRIOR FILING DATE: 2000-10-17
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/ PRIOR FILING DATE: 2000-10-17
/ PRIOR APPLICATION NUMBER: 60/241,243
/ PRIOR FILING DATE: 2000-10-17
/ PRIOR APPLICATION NUMBER: 60/242,152
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/242,482
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/242,611
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/242,612
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/242,880
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: 60/242,881
/ PRIOR FILING DATE: 2000-10-24
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 160
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 7
/ LENGTH: 2895
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-09-981-151A-7

Alignment Scores:
Pred. No.: 0
Score: 5236.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 10
Gaps: 0
Length: 2895
Matches: 952
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-09-981-151D-8 (1-952) x US-09-981-151A-7 (1-2895)
QY 1 MetLysProArgAlaArgGlyTrpArgGlyLeuAlaAlaLeuTrpMetLeuLeuAlaGln 20
DB 10 ATGAAGCCCCCGCGCGCGCGATGGCGGCTTGGCGGATGCTGTTGGCGCAG 69
QY 21 ValAlaGluGlnValSerProGlyArgSerHisGlnArgGlyAsnArgGlySerGlyGln 40
DB 70 GTGGCCGAGCAGGTGAGTCCCGGGCGCTCCCAACAGCGCGAAACCGGGTCCGGACAG 129
QY 41 LeuGluAlaSerProProArgLeuLeuSerArgGlyProArgArgLeuThralaMetSer 60
DB 130 CTGAGAGCGAGTCCCCCGCGCTCTCCCGCGGAGACCCCGCTCTCACCGGATGTG 189
QY 61 ProLeuPheSerAlaGlyThrCysValArgHisGlyThrArgSerGlySeralatTrpGlu 80
DB 190 CCGCTGTTTCCGACGACGACCTCGCTGCGGCATGGGACCCGCGGACGCGCTGGAG 249
QY 81 ProGluArgProAlaSerSerSerThrArgGlyAlaAlaGlyLeuAspGlyLysGlyArg 100
DB 250 CCCGAGCGTCCGCGCTCTCTCTTCCACCCGCGGAGCGCGCGGCTGGATGAAAAAGGCGG 309

QY 101 AspMetAspGluAlaGlyAsnHisArgSerGlnGlnThrAsnThrGlyThrGluAsnGln 120
DB 310 GACATGATGAAAGCTGGAAACCATCGTTCTCAGCAAACTTAACACAGGAACAGAAACCAG 369
QY 121 ThrLeuHisValLeuThrGlnTyrAspLeuValSeralatTyrGluValAspHisArgGly 140
DB 370 ACACTGCATGTTCTCACTCAATATGACTGTCTCTGCTTACGAGGTTACCAAGGGGC 429
QY 141 AspTyrValSerHisGluIleMetHisHisGlnArgArgArgAlaValAlaValSer 160
DB 430 GATTACGTGTCCTCCATGAAATCATGCACCATCAGCGCGGAGAGAGCAGTGGCGGTGCC 489
QY 161 GluValGluSerLeuHisLeuArgLeuLysGlyProArgHisAspPheHisMetAspLeu 180
DB 490 GAGGTGAGTCTCTTCACTTCGGCTGGAAGGCCCCAGGACAGACTTCCACATGATCTG 549
QY 181 ArgThrSerSerSerLeuValAlaProGlyPheIleValGlnThrLeuGlyLysThrGly 200
DB 550 AGGACTTCCAGCAGCCTTAGTGGCTCTGGCTTTATTGTGCAGACGTTGGGAAAAAGACAGGC 609
QY 201 ThrLysSerValGlnThrLeuProProGluAspPheCysPheTyrGlnGlySerLeuArg 220
DB 610 ACTAAGTCTGTGCAGACTTTTACCGCAGAGACTTCTGTTTCTATCAAGGCTCTTTGGCGA 669
QY 221 SerHisArgAsnSerProSerHisGlyGlyLysPheCysGluGlySerThrArgThrLeu 240
DB 670 TCACACAGAAACTCGCCATCGCATGGAGGAAGTTCTGTGAGGGCTCCACTCGCACTCTG 729
QY 241 LysLeuCysAsnSerGlnLysCysProArgAspSerValAspPheArgAlaAlaGlnCys 260
DB 730 AAGCTTGCACACAGTCAAGAAATGTCCCGGACAGTGTGACTTCCGTGCTCAGTGT 789
QY 261 AlaGluHisAsnSerArgArgPheArgGlyArgHisTyrLysTrpLysProTyrThrGln 280
DB 790 GCCGAGCAACAACAGCAGATTCAGAGGGCGGCACACTTAACAATGGAAGCTTACACTCA 849
QY 281 ValGluAlaAspLeuCysLysLeuTyrCysIleAlaGluGlyPheAspPhePhePheSer 300
DB 850 GTAGAGCCGACTTATGCAAACTTACTGTATGCGAAGAGATTGATTCTTCTTCT 909
QY 301 LeuSerAsnLysValLysAspGlyThrProCysSerGluAspSerArgAsnValCysIle 320
DB 910 TTGTCAATTAAGTCAAGATGGAGTCCATGCTCGGAGATAGCCGTAAATGTTGTATA 969
QY 321 AspGlyIleCysGluLeuSerValValSerThrSerAlaHisMetProGlnProProLys 340
DB 970 GATGGATATGTGAGCTCAGTGTGTGTCCACATCTGCGCACATGCCCAAGCTCCCAAG 1029
QY 341 GluAspLeuPheIleLeuProAspGluTyrLysSerCysLeuArgHisLysArgSerLeu 360
DB 1030 GAAAGCTCTTCACTTGTCCAGATGAGTAAAGTCTTGTACGGCATAAAGCGCTCTCTT 1089
QY 361 LeuArgSerHisArgAsnGluGluLeuAsnValGluThrLeuValValAspLysLys 380
DB 1090 CTGAGGTCCCATAGAAATGAAGAACTGAACGTGAGACCTTGTGTGTGTCGACAAAAG 1149
QY 381 MetMetGlnAsnHisGlyHisGluAsnIleThrThrTyrValLeuThrIleLeuAsnMet 400
DB 1150 ATGATGCAAAACCATGCGCATGAAATATCACCACTTACGTCTCACGATTACTCAACTG 1209
QY 401 ValSeralaleuPheLysAspGlyLeuMetGlyLysAspGlyThrArgHisAspHisAla 420
DB 1210 GTATCTGCTTTATTCAAAAGATGATGATGGGAAAGATGGAGTCTGTCATGACCAAGCC 1269
QY 421 IleLeuLeuThrGlyLeuAspIleCysSerTrpLysAsnGluProCysAspThrLeuGly 440
DB 1270 ATCTTACTGACTGTGTGATATATATGTTCTCGAAGAAATGAGCCCTGTGACACTTGGGA 1329
QY 441 PheAlaProIleSerGlyMetCysSerLysTyrArgSerCysThrIleAsnGluAspThr 460
DB 1330 TTTCACCCCATTAAGTGAATGTGTAGTAAATATATCGCAGCTGCACGATTAATGAAGATACA 1389

QY	461	G1YLeuGLYLeuAlaphethr11eAlah1sg1uSerGLYh1sAsnPhedGLYmE11eh1s	480
Db	1390	GGTCTTGgACTGGCCCTTCAcCAATTGGCCATgAGTCTGGACACAACTTTGGCATgATTCA1	1449
QY	481	AspGLYGLUGLYAsnMetCysLYsLYsSerGLUGLYAsn11eMetSerProthrLeuAla	500
Db	1450	GATGGAGAGGGAAcATgTGTA AAAAGTCCGAGGGCAcATCATgTCCCTCACTTGGCA	1509
QY	501	GLYArgAsnGLYValPheSerTrpSerProCysSerArgGLInTYrLeuH1sLYsPheLeu	520
Db	1510	GGAAGCAATGGAGTCTTCTCTGGTCAcCCTGCAGCCGCGCAGTATCTACACAA1TTTCTA	1569
QY	521	SerThrAlaGLInAla11eCysLeuAlaAspGLInProLYsProValLYsGLInTYrLYsTYr	540
Db	1570	AGCAcCGCTCAAGCTATCTGCTTGTCTGATCAcCCAAAGCCTGTGAAGGAATAcAAGTAT	1629
QY	541	ProGLULysLeuProGLYGLUleuTYrAspAlaAsnThrgInCysLYsTrpGLInPheGLY	560
Db	1630	CCTGAGAAATTTGCCAGGAATTAATgATGATGC AAACAcACAGTGC AAAGTGGCAGTTCCGA	1689
QY	561	GLULysAlaLYsLeuCysMetLeuAspPheLYsAsp11eCysLYsAlaLeuTrpCys	580
Db	1690	GAGAAAGCCAAgCTCTGCATGCTGGACTTTAAAAAGAcATCTGTAAAGCCCTGTGTGC	1749
QY	581	H1sArg11eGLYArgLYsCysGLInThrLYsPheMetProAlaAlaGLUGLYThr11eCys	600
Db	1750	CATGTATTGGAGGAATGTGAGACTAAATTTATGCCAGAcAGAGAAGGCACAA1TTGT	1809
QY	601	GLYH1sAspMetTrpCysArgGLYGLInCysValLYsTYrGLYAspGLUGLYProLYs	620
Db	1810	GGGCATGACATGTGGTGCCGGGGAGGACAGTGTGTGAATATGTGTATGAAGGCCCAAG	1869
QY	621	ProThrH1eGLYH1sTrpSerAspTrpSerSerTrpSerProCysSerArgThrCysGLY	640
Db	1870	CCCACCCATGGCCACTGGTGGACTGTTCTTGTGTCCCATGCTCCAGGACCTGGCGGA	1929
QY	641	GLYGLYValSerH1sArgSerArgLeuCysThraSnProLYsProSerH1eGLYLYs	660
Db	1930	GGGGAGTATCTCATAGAGTGCCTCTGCACCAACCCCAAGCCATGCATGGAGGGAAAG	1989
QY	661	PheCysGLUGLYSerThraArgThrLeuLYsLeuCysAsnSerGLInLYsCysProArgAsp	680
Db	1990	TTCTGTGAGGGCTCCACTCGCACTGTAAgCTCTGC AAACAGTCA GAATGTCCCGGAC	2049
QY	681	SerValAspPheArgAlaAlaGLInCysAlaGLInH1sAsnSerArgArgPheArgGLYArg	700
Db	2050	AGTGTGACTTCCGTCTGCTCAgTGTGCCAGACAAcACAGACAGATTCAGAGGGCGG	2109
QY	701	H1sTYrLYsTrpLYsProTYrThrgInValGLUAspGLInAspLeuCysLYsLeuTYrCys	720
Db	2110	CACTACAAGTGAAGCCCTTACACTCAAGTAGAAGATCAAGACTTATGCAAACTCTACTGT	2169
QY	721	11eAlaGLUGLYPheAspPhePhePheSerLeuSerAsnLYsValLYsAspGLYThrPro	740
Db	2170	ATCGCAGAAAGATTGATTCTTCTTTCTTTGTCTCAATAAAAGTCAAAAGATGGGACTCCA	2229
QY	741	CysSerGLUAspSerArgAsnValCys11eAspGLY11eCysGLUArgValGLYCysAsp	760
Db	2230	TGCTCGAGGATAGCCGTAAATGTTTGTATAGATGGGATATGTGAGAGAGTGGATGTGAC	2289
QY	761	AsnValLeuGLYSerAspAlaValGLUAspValCysGLYValCysAsnGLYAsnAsnSer	780
Db	2290	AATGTCTTGATCTGATGCTGTGTAAGACGCTGTGTGGGTGTGTAAcGGGAATACTCA	2349
QY	781	AlaCysThr11eH1sArgGLYleuTYrThrLYsH1sH1sH1eThraSnGLInTYrTYrH1s	800
Db	2350	GCCTGCACGATTCACAGGGGTCTCTACACCAAGCAcCACCAcCAACcAGTATTATCAC	2409
QY	801	MetValThr11eProSerGLYAlaArgSer11eArg11eTYrGLUeMetAsnValSerThr	820
Db	2410	ATGGTCAcCATTCCTTCTGTGAGCCCGAGTATCCGATCTATGAATGAACGTCTCTACC	2469
QY	821	SerTYr11eSerValArgAsnAlaLeuArgArgTYrTYrLeuAsnGLYH1sTrpThraVal	840

Db	2470	TCCTACATTTCTGTGCGCATGCCCCAGAAAGTACTACTGAATGGGCACTGGACCGTG	2529
QY	841	AspTrpProGlyArgTyrIysPheSerGlyThrThrPheAspTyrArgSerTyrAsn	860
Db	2530	GACTGGCCCGGCGCGGTACAAATTTTCGGGCACTACTTGCACTACAGACGGTCTATAT	2589
QY	861	GluProGluAsnLeuIleAlaThrGlyProThrAsnGluThrLeuIleValGluLeu	880
Db	2590	GAGCCCGAAGAACTTAATCGCTACTGACCAACCAACGAGCACTGATTGTGAGCTGCTG	2649
QY	881	PheGlnGlyArgAsnProGlyValAlaTyrGluTyrSerMetProArgGluGlyThrGlu	900
Db	2650	TTTCAGGGAAGAAACCCGGGTGTTCCTGGGAATACTCATGCTCGCTTGGGGACCGAG	2709
QY	901	LysGlnProProAlaGlnProSerTyrThrTrpAlaIleValArgSerGluCysSerVal	920
Db	2710	AAGCAGCCCCCTGCCCCAGCCCACTACACTGGGCCATCGTGCCTCTGAGTGTCCGTG	2769
QY	921	SerCysGlyGlyGlyArgCysLeuProValleuLeuGluAlaAlaCysGlnProSer	940
Db	2770	TCCTGCGGAGGGGGTAGTGTCCTTCCAGTGTCTGCTCTGGAGGAGCAGCATGTCCGCTTCA	2829
QY	941	AlaThrAlaTyrIleAlaLeuAlaPheLeuGluSer	952
Db	2830	GCCACTGCGTACATTGCACCTGCTTCTTGAATCC	2865

RESULT 2

US-09-981-151A-1

Sequence 1, Application US/09981151A

Publication No. US20030212256A1

GENERAL INFORMATION:

APPLICANT: Edinger, Shlomit R

APPLICANT: Gerlach, Valerie

APPLICANT: MacDougall, John R

APPLICANT: Malyankar, Muriel M

APPLICANT: Smithson, Glenda

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APPLICANT: Kekuda, Ramesh

APPLICANT: Spytek, Kimberly A

APPLICANT: Gangoli, Esba A

APPLICANT: Fernandes, Elma R

APPLICANT: Gorman, Linda

TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

FILE REFERENCE: 21402-168

CURRENT APPLICATION NUMBER: US/09/981,151A

CURRENT FILING DATE: 2001-10-16

PRIOR APPLICATION NUMBER: 60/241,040

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/241,058

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/241,063

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/241,243

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/242,152

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/242,482

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/242,611

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/242,612

; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,880
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/242,881
; PRIOR FILING DATE: 2000-10-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2997
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (857)..(858)
; OTHER INFORMATION: wherein n is an a or t or c or g.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2383)
; OTHER INFORMATION: wherein n is an a or t or c or g.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2983)
; OTHER INFORMATION: wherein n is an a or t or c or g.
US-09-981-151A-1

Alignment Scores:
Pred. No.: 0 Length: 2997
Score: 5110.00 Matches: 940
Percent Similarity: 94.67% Conservative: 1
Best Local Similarity: 94.57% Mismatches: 3
Query Match: 97.59% Indels: 50
DB: 10 Gaps: 4

US-09-981-151d-8 (1-952) x US-09-981-151A-1 (1-2997)

QY 1 MetLysProArgAlaArgGlyTrpArgGlyLeuAlaLeuTrpMetLeuAlaGln 20
DB 10 ATGAAGCCCCCGCGCGCGGATGGCGGGCTTGCGCGGCTGTGGATGCTTTGGCGCAG 69
QY 21 ValAlaGlnValSerProGlyArgSerHisGlnArgGlyAsnArgGlySerglyGln 40
DB 70 GTGGCCGAGCAGTAGTCCCGGGCGCTCCCAACGCGGAAACCGCGGTCGCGACAG 129
QY 41 LeuGluAlaSerProProArgGluLeuSerArgGlyProArgArgLeuThrAlaMetSer 60
DB 130 CTGAGGCGAGTCCCGCGGCTCTCTCCCGGAGACCCCGCTCTCACCGCATGTGCG 189
QY 61 ProLeuPheSerAlaGlyThrCysValArgHisGlyThrArgSerglySeraAlaTrpGlu 80
DB 190 CCGCTGTTTCCGACAGGACCTGCGCGCAATGGAGACCCGACGCGCAGCCTGGAG 249
QY 81 ProGluArgProAlaSerSerSerSerThrArgGlyAlaAlaGlyLeuAspGlyLySgLYArg 100
DB 250 CCCGAGCGTCCCGCGTCTCTCTCCACCCGCGGAGCGCGCGCTGGATGAAAGGCGG 309
QY 101 AspMetAspGluAlaGlyAsnHisArgSerglnGlnThrAsnThrGlyThrGluAsnGln 120
DB 310 GACATGATGAAGCTGGAACCATCGTTCTCAAGCAAACTAACAAGAAACCAACAA 369
QY 121 ThrLeuHisValLeuThrGlnTyArgPleuValSerAlaTyrgluValAspHisArgGly 140
DB 370 ACACTGCATGTTCTCACTCAATATGACCTGTCTCTGCTTCAAGGTTGACCAAGGGGC 429
QY 141 AspTyrValSerHisGluLeuMetHisHisGlnArgArgArgAlaValAlaValSer 160
DB 430 GATTACGTGTCCCATGAATCATGCACCATCAGCGGCGGAGAAAGACAGTGGCGGTCC 489
QY 161 GluValGluSerLeuHisLeuArgLeuLySgLYProArgHisAspPheHisMetAspLeu 180
DB 490 GAGGTGAGTCTCTTCACTTCCGCTGAAGGCCCCAGGACGACTTCCACATGATGATCTG 549
QY 181 ArgThrSerSerSerLeuValAlaProGlyPheIleValGlnThrLeuGlyLySThrGly 200

DB 550 AGGACTTCCAGCAGCCTAGTGCTCTGCTTTATTGTGACAGACGTGGGAAAGACAGGC 609
QY 201 ThrLysSerValGlnThrLeuProProGluAspPheCysPheTyrglnGlySerLeuArg 220
DB 610 ACTAGTCTGTGACACTTACCGCCAGAGACTTCTGTTCATCAAGGCTCTTGGCGA 669
QY 221 SerHisArgAsnSerProSerHisGlyGlyLySPhCysGluGlySerThrArgThrLeu 240
DB 670 TCACACAGAACTCGCCATCGCATGAGGAAAGTTCTGTGAGGGCTCCACTCGCACTCTG 729
QY 241 LysLeuCysAsnSerGlnLyS CysProArgAspSerValAspPheArgAlaAlaGlnCys 260
DB 730 AAGCTTGCAACAGTCAGAAATGTCCCCGGGACAGTGTGACTTCCGTGCTCAAGTGT 789
QY 261 AlaGluHisAsnSerArgArgPheArgGlyArgHisTyrglySTrpLySProTyrgln 280
DB 790 GCCGAGCAACAAGACGATTCAGAGGGCGGCACTACAAAGTGGAAGCCTTACACTCAA 849
QY 281 ValGluAlaAspLeuCysLySLeuTyrglySleAlaGluGlyPheAspPhePheSer 300
DB 850 GTAGAAGNNGACTTATGCAAACTACTGTATCGCAGAAGATTGATTCTTCTTTCT 909
QY 301 LeuSerAsnLySValLySAspGlyThrProCysSerglyAspSerArgAsnValCysIle 320
DB 910 TTGTCAATAAAGTCAAAAGATGGGACTTCATGCTCGGAGATAGCCGTAATGTTGTATA 969
QY 321 AspGlyIleCysGluLeuSerValSerThrSeraHisMetProGlnProProLyS 340
DB 970 GATGGATATGTGAGCTAGTGTGTGCCACATCTGCGCACATGCCGCCCTCCCAAG 1029
QY 341 GluAspLeuPheIleLeuProAspGlyTyrglySerglySleuArgHisLySArgSerLeu 360
DB 1030 GAAGACCTTTCATCTTGCCAGATGAGTATTAAGTCTTGCTTACGGCATTAAGCGCTCTT 1089
QY 361 LeuArgSerHisArgAsnGluGluLeuAsnValGluThrLeuValValAspLyS 380
DB 1090 CTGAGGTCCCATGAATGAAGAACTGAACGTGAGACCTTGGTGTGTCGACAAAG 1149
QY 381 MetMetGlnAsnHisGlyHisGluAsnIleThrTyrglyValLeuThrIleLeuAsnMet 400
DB 1150 ATGATGCAAAACCATGGCCATGAATAATACACCACTTACGTCTCACGATACTCAACATG 1209
QY 401 ValSerAlaLeuPheLySAsp----- 407
DB 1210 GTATCTGCTTTATTCAAAAGATGAACAATAAGAGAAACATCAACATTGCAATTGTAGT 1269
QY 407 ----- 407
DB 1270 CTGATTCTTTAGAAAGATGAACAGCAGCACTGTGATTAAGTCACACGACACACACC 1329
QY 408 -----GlyLeuMetGlyLySAspGlyThrArgHisAsp 418
DB 1330 TTAAGTAGCTTCTGCCAGTGGCAGTCTGGAATTGATGGGAAAGATGGACTCGTCATGAC 1389
QY 419 HisAlaIleLeuLeuThrGlyLeuAspIleCysSerTrpLySAsnGluProCysAspThr 438
DB 1390 CACGCCATCTTACTGACTGTCTGATATATGTTCTTGGAAGAAATGAGCCCTGTGACACT 1449
QY 439 LeuGlyPheAlaProIleSerGlyMetCysSerLyTyrglySerglySThrIleAsnGlu 458
DB 1450 TTGGGATTTGCACCCATTAAGTGAATGTGTAATAATATCGCAGCTGCACGATTAAATGAA 1509
QY 459 AspThrGlyLeuGlyLeuAlaPheThrIleAlaHisGluSerglyHisAsnPheGlyMet 478
DB 1510 GATACAGTCTTGAGCTGGCTTACCATTTGCCATGTCCCATGAGTCTGGACAACTTGGCAG 1569
QY 479 IleHisAspGlyGluGlyAsnMetCysLySlySerglyGlyAsnIleMetSerProThr 498
DB 1570 ATTCAATGATGAGAAAGGAACATGTGTAAAAAGTCGAGGGCAACATCATGTCCCTTACA 1629
QY 499 LeuAlaGlyArgAsnGlyValPheSerTrpSerProCysSerArgGlnTyrglySleuHisLyS 518

DB 1630 TTGGCAGACGCAATGAGTCTTCTCTCTGTCACCTCGACGCCCGCATATCTACACAA 1689
QY 519 PheLeuSerThrAlaGlnAlaIleCysLeuAlaAspGlnProLysProValLysGluTyr 538
DB 1690 TTTCTAAGACACCGCTCAAGCTATCTGCTGTGATCAGCCAAAGCCTGTGAAGAAATAC 1749
QY 539 LysTyrProGluLysLeuProGlyGluLeuTyrAspAlaAsnThrGlnCysLysTyrGln 558
DB 1750 AAGTATCCTGAGAAATGGCAGAGAAATTATATGATGCAAACACACAGTGCAGTGGCAG 1809
QY 559 PheGlyGluLysAlaLysLeuCysMetLeuAspPheLysLysAspIleCysLysAlaLeu 578
DB 1810 TTCGAGAGAAAGCCAAGCTCTGCATGCTGACTTAAAGACATCTGTAAGCCCTG 1869
QY 579 TrpCysHisArgIleGlyArgLysCysGluThrLysPheMetProAlaAlaGluGlyThr 598
DB 1870 TGGTGCCATCGTATGGAGGAATGTGAGACTAATTATGCGCAGCAGAGAGCACACA 1929
QY 599 IleCysGlyHisAspMetTrpCysArgGlyGlyGlnCysValLysTyrGlyAspGluGly 618
DB 1930 ATTTGTGGGCATGACATGTGTGTCGGGAGAGACAGTGTGTAATATGTGTGTAAGGC 1989
QY 619 ProLysProThrHisGlyHisIleTrpSerAspTrpSerSerTrpSerProCysSerArgThr 638
DB 1990 CCCAAGCCCCACCCATGGCCACCTGGTCCGACTGGTCTTCTTGGTCCCATGCTCCAGACC 2049
QY 639 CysGlyGlyGlyValSerHisArgSerArgLeuCysThrAsnProLysProSerHisGly 658
DB 2050 TCGCGAGGGGAGTATCTCATAGAGAGTCCGCTCTGCACCAACCCCAATCCATCCATGGA 2109
QY 659 GlyLysPheCysGlyGluGlySerThrArgThrLeuLysLeuCysAsnSerGlnLysCysPro 678
DB 2110 GCGAAGTTCTGTGAGGGGCTCCACTCGCACTCTGAAAGCTCTGCACACAGTACAGAAATGTC 2169
QY 679 ArgAspSerValAspPheArgAlaAlaGlnCysAlaGluHisAsnSerArgArgPheArg 698
DB 2170 CCGGACAGTGTGCACTTCCGTGCTGCTCAGTGTGCCGAGCACACAGCAGACGATTGAGA 2229
QY 699 GlyArgHisTyrLysTrpLysProTyrThrGlnValGluAspGlnAspLeuCysLysLeu 718
DB 2230 GGGCGGCACCTACAAGTGAAGCCT-----CAGGACTTATGCAAACTC 2271
QY 719 TyrCysIleAlaGluGlyPheAspPhePheSerLeuSerAsnLysValLysAspGly 738
DB 2272 TACTGTATCGCAGAGGATTGATTCTTCTTTCTTTGTCAATAAAGTCAAAAGATGGG 2331
QY 739 ThrProCysSerGluAspSerArgAsnValCysIleAspGlyIleCysGluArgValGly 758
DB 2332 ACTCCATGCTCGAGGATAGCCGTAATGTTGTATAGATGGGATATGTGAG--NTTGA 2388
QY 759 CysAspAsnValLeuGlySerAspAlaValGluAspValCysGlyValCysAsnGlyAsn 778
DB 2389 TGTGACAAATGTCCTTGATCTGTGATGCTGTTGAAGACGTCTGTGGGTGTGTAACGGGAAT 2448
QY 779 AsnSerAlaCysThrIleHisArgGlyLeuTyrThrLysHisHisIleThrAsnGlnTyr 798
DB 2449 AACTCAGCCTGCACGATTCAACAGGGGTCTCTACACCAAGCACCAACCAACCAAC--CAT 2505
QY 799 TyrHisMetValThrIleProSerGlyAlaArgSerIleArgIleTyrGluMetAsnVal 818
DB 2506 TATCACATGTCACCATTCCTTCTGAGGCCCGGAGTATCCGCATCTATGAATGAAGAACGTC 2565
QY 819 SerThrSerTyrIleSerValArgAsnAlaLeuArgArgTyrTyrLeuAsnGlyHisIleTrp 838
DB 2566 TCTACCTCCTACATTTCTGTGCGCAATGCCCTCAGAAAGTACTACTGAATGGCACTGG 2625
QY 839 ThrValAspTrpProGlyArgTyrLysPheSerGlyThrThrPheAspTyrArgArgSer 858
DB 2626 ACCGTGACTGGCCCGCGGTACAAATTTTGGGCACTACTTTCGACTACAGCGGTCC 2685
QY 859 TyrAsnGluProGluAsnLeuIleAlaThrGlyProThrAsnGluThrLeuIleValGlu 878
DB 2686 TATTAATGAGCCCGAAGAACTTAATCGCTACTGACCAACCAACGAGACACTGATTGTGAG 2745

QY 879 LeuLeuPheGlnGlyArgAsnProGlyValAlaTrpGluTyrSerMetProArgLeuGly 898
DB 2746 CTGCTGTTTCAGGGAAGAACCCGGGTGTTCCTGGGAATACCTCATGCCCTGTGGGG 2805
QY 899 ThrGluLysGlnProProAlaGlnProSerTyrThrTrpAlaIleValArgSerGluCys 918
DB 2806 ACCGAGAGCAGCCCCCTCGCCAGCCCAAGTACACTTGGGCCATCGTCCGCTGTAGTGC 2865
QY 919 SerValSerCysGlyGlyGlyArgCysLeuProValLeuLeuLeuGluAlaAlaCysGln 938
DB 2866 TCCGTGCTCGCGGAGGGGTAGGTGCTTCCAGTGTCTGCTGAGGCGACATGTGAG 2925
QY 939 ProSerAlaThrAlaTyrIleAlaLeuAlaPheLeuGluSer 952
DB 2926 CTTCAAGCCACTGCGTACATTGCACCTGACCTTTCTGAATCC 2967
RESULT 3
US-09-981-151A-3
; Sequence 3, Application US/09981151A
; Publication No. US20030212256A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Gerlach, Valerie
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Muriel M
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A
; APPLICANT: Stone, David J
; APPLICANT: Gunther, Erik
; APPLICANT: Ellerman, Karen
; APPLICANT: Shimkets, Richard A
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Guo, Xiaojia
; APPLICANT: Patturajan, Meera
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Burgess, Catherine E
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Gangolli, Esma A
; APPLICANT: Fernandes, Elma R
; APPLICANT: Gorman, Linda
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-168
; CURRENT APPLICATION NUMBER: US/09/981,151A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 60/241,040
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,058
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,063
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,243
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/242,152
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/242,482
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,611
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,612
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,880
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/242,881
; PRIOR FILING DATE: 2000-10-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2433


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:      TYPE: DNA
:      ORGANISM: Homo sapiens
US-09-981-151A-3

Alignment Scores:
Pred. No.:      0      Length:      2433
Score:      4103.50      Matches:      774
Percent Similarity:      82.16%      Conservative:      9
Best Local Similarity:      81.22%      Mismatches:      7
Query Match:      78.37%      Indels:      163
DB:      10      Gaps:      8

US-09-981-151D-8 (1-952) x US-09-981-151A-3 (1-2433)

QY      1 MetLysProAlaGAlaArgGlyTTPArgGlyLeuAlaAlaLeuTrpMetLeuLeuAlaGln 20
DB      31 ATGAAGCCCCCGCGCGCGGATGGCGGGGCTGGCGGCGCTGTGATGCTGCGCGCAG 90
QY      21 ValAlaGluGlnValSerProGlyArgSerHisGlnArgGlyAsnArgGlySerGlyGln 40
DB      91 GTGGCCGAGCAGGTGAGTCCCGGGCGCTCCACACGCGGAAACCGCGGTCGCGACAG 150
QY      41 LeuGluAlaSerProProArgLeuLeuSerArgGlyProArgArgLeuThrAlaMetSer 60
DB      151 CTGGAGCGCAGTCCCCCGCGGCTCTCTCCCGGAGACCCCGCGCTCTCACCGCGATGTCG 210
QY      61 ProLeuPheSerAlaGlyThrCysValArgHisGlyThrArgSerGlySerAlaTrpGlu 80
DB      211 CCGCTGTTTCCGACAGGACACCTGCGCCATGGGACCCGCAAGCGCAGCGCCTGGAG 270
QY      81 ProGluArgProAlaSerSerSerThrArgGlyAlaAlaGlyLeuAspGlyLysGlyArg 100
DB      271 CCCGAGCGTCCCGCGTCTCTCTCCACCCGCGAGCGGCGGCGCTGATGAAAGGCGG 330
QY      101 AspMetAspGluAlaGlyAsnHisArgSerGlnGlnThrAsnThrGlyThrGluAsnGln 120
DB      331 GACATGATGAAGCTGGAACCATCGTTCTCAACAACATAACACAGAAAGAAACCAA 390
QY      121 ThrLeuHisValLeuThr-----GlnTyArgPheValSerAlaTyrgluValAspHisArg 139
DB      391 ACACTGCATGTTCTCTCACTCGTAATATGACCTGTCTCTGCTTACGAGTTGACCAAG 450
QY      140 GlyAspTyrValSerHisGluIleMetHisHisGlnArgArgArgAlaValAlaVal 159
DB      451 GGCATTACGTGTCCTCCATGAATCATGACACCATCAGCGGCGGAGAAAGAGAGTGGCGGTG 510
QY      160 SerGluValGluSerLeuHisLeuArgLeuLysGlyProArgHisAspPheHisMetAsp 179
DB      511 TCCGAGGTGAGTCTCTTCACTTCCTCGGTGAAGGCCCCAGGCAAGCACTTCCACATGAT 570
QY      180 LeuArgThrSerSerSerSerLeuValAlaProGlyPheIleValGlnThrLeuGlyLysThr 199
DB      571 CTGAGGACTTCCAGACGCTAGTGGCTCTCGGCTTATTATGTGCAGACGTTGGGAAAGACA 630
QY      200 GlyThrLysSerValGlnThrLeuProProGluAspPheCysPheTyrGlnGlySerLeu 219
DB      631 GGCACATAAGTCTGTGCAGACTTTACCGCCAGAGGACTTGTGTTTCTATCAAGGCTCTTTG 690
QY      220 ArgSerHisArgAsnSerProSerHisGlyLysLysPheCysGluGlySerThrArgThr 239
DB      691 CGATCACACAGAAACTCCCATCGCATGGAGGAAGTTCTGTGAGGGGCTCCACTCGCACT 750
QY      240 LeuLysLeuCysAsnSerGlnLysCysProArgAspSerValAspPheArgAlaAlaGln 259
DB      751 CTGAAGCTCTGCAACAGTCAGAATGTCCCGGGACAGTGTGACTTCCGTGCTGCTCAG 810
QY      260 CysAlaGluHisAsnSerArgArgPheArgGlyArgHisTyrLysTrpLysProTyrThr 279
DB      811 TGTGCCGAGACAACAAGCAGATTCAGAGGGCGGCACTACAAGTGGAACCTTACACT 870
QY      280 GlnValGluAlaAspLeuCysLysLeuTyrCysIleAlaGluGlyPheAspPhePhePhe 299
DB      871 CAAGTAGAACAGGACTTATGCAAACTCTACTGTATCCGAGAAAGATTGATTCTTCTTT 930
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QY      300 SerLeuSerAsnLysValLysAspGlyThrProCysSerGluAspSerArgAsnValCys 319
DB      931 TCTTGTCAATAATAAGTCAAAAGATGGACTCCATGCTCGAGAGATAGCGTAAATGTGTGT 990
QY      320 IleAspGlyIleCysGluLeuSerValSerThrSerAlaHisMetProGlnProPro 339
DB      991 ATAGATGGATATGTAG-----ATGCCCCAGCCTCCC 1023
QY      340 LysGluAspLeuPheIleLeuProAspGluTyrLysSerCysLeuArgHisLysArgSer 359
DB      1024 AAGGAGACCTCTTCACTTCTGCCAGATGAGTATAGTCTTGCTTACGGCATTAAGCGCTCT 1083
QY      360 LeuLeuArgSerHisArgAsnGluGluLeuAsnValGluThrLeuValValValAspLys 379
DB      1084 CTTCGTAGGTCCCATAGAAATGAAGAACTGAACGTGAGACCTTGGTGTGTCGACAA 1143
QY      380 LysMetMetGlnAsnHisGlyHisGluAsnIleThrThrTyrValLeuThrIleLeuAsn 399
DB      1144 AAGATGATGCAAAACCATGGCCATGAATAATATCACCACTTACGTGCTCAGATACTCAAC 1203
QY      400 MetValSerAlaLeuPheLysAspGlyLeuMetGlyLysAspGlyThrArgHisAspHis 419
DB      1204 ATGATATCTGCTTATATTCAAAGATGGAACAATAGGA----- 1239
QY      420 AlaIleLeuLeuThrGlyLeuAspIleCysSerTrpLysAsnGluProCysAspThrLeu 439
DB      1239 ----- 1239
QY      440 GlyPheAlaProIleSerGlyMetCysSerLysTyrArgSerCysThrIleAsnGluAsp 459
DB      1239 ----- 1239
QY      460 ThrGlyLeuGlyLeuAlaPheThrIleAlaHisGluSerGlyHisAsnPheGlyMetIle 479
DB      1239 ----- 1239
QY      480 HisAspGlyGluGlyAsnMetCysLysLysSerGluGlyAsnIleMetSerProThrLeu 499
DB      1240 -----GGAACATC---AACATTGCAATT 1260
QY      500 AlaGlyArgAsnGlyValPheSerTrpSerProCysSerArgGlnTyrLeuHisLysPhe 519
DB      1261 GTAGT----- 1266
QY      520 LeuSerThrAlaGlnAlaIleCysLeuAlaAspGlnProLysProValLysGluTyrLys 539
DB      1266 ----- 1266
QY      540 TyrProGluLysLeuProGlyGluLeuTyrAspAlaAsnThrGlnCysLysTrpGlnPhe 559
DB      1266 ----- 1266
QY      560 GlyGluLysAlaLysLeuCysMetLeuAspPheLysLysAspIleCysLysAlaLeuTrp 579
DB      1267 -----CTGATTCCTTGAAGATGAACAGACATCTGTAAAGCCCTGTGG 1311
QY      580 CysHisArgIleGlyArgLysCysGluThrLysPheMetProAlaAlaGluGlyThrIle 599
DB      1312 TGCCATCGTATTGGAAGGAATGTAGACTAAATTATGCCAGCAGAGAAAGGCACAAATT 1371
QY      600 CysGlyHisAspMetTrpCysArgGlyGlyGlnCysValLysTyrGlyAspGlyGlyPro 619
DB      1372 TGTGGCATGACATGTGGTGCCGGGAGGACAGTGTGTGAATATGTGATGAAGGCCCC 1431
QY      620 LysProThrHisGlyHisIleTrpSerAspTrpSerSerTrpSerProCysSerArgThrCys 639
DB      1432 AAGCCCAACCATGGCCACTGTGCGACTGTCTTGTGTGCCCATGCTCCAGGACCTGC 1491
QY      640 GlyGlyGlyValSerHisArgSerArgLeuCysThrAsnProLysProSerHisGlyGly 659
DB      1492 GGAGGGGAGTATCATAGAGTGCCTCTGCACCAACCCAGGCCATCGCATGGAGG 1551
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QY 660 LysPheCysGluGlySerThrArgThrLeuLysLeuCysAsnSerGlnLysCysProArg 679
      |||||||
Db 1552 AAGTCTGTGAGGGCTCCACTCGCACTCTGAAGCTCTGCAACAGTCAGAATATGCCCGG 1611

QY 680 AspSerValAspPheArgAlaAlaGlnCysAlaGlnHisAsnSerArgArgPheArgGly 699
      |||||||
Db 1612 GACAGTGTGACTTCGGTGTGCTCAGTGTGCCAGACAAACAGACAGCATTCAGAGGG 1671

QY 700 ArgHisTyrLysTyrLysProTyrThrGlnValGluAspGlnAspLeuCysLysLeuTyr 719
      |||||||
Db 1672 CGGCACTACAAGTGAAGCCT-----CAGGACTTATGCAACTCTAC 1713

QY 720 CysIleAlaGluGlyPheAspPhePheSerLeuSerAsnLysValLysAspGlyThr 739
      |||||||
Db 1714 TGTATCGCAGAGGATTGATTCTTCTTCTTCTTGTCAATAAGTCAAGATGGGACT 1773

QY 740 ProCysSerGluAspSerArgAsnValCysIleAspGlyIleCysGluArgValGlyCys 759
      |||||||
Db 1774 CCATGCTCGGAGGATAGCCGTAATGTTGTATAGATGGGATATGTGAG-----GGATGT 1827

QY 760 AspAsnValLeuGlySerAspAlaValGluAspValCysGlyValCysAsnGlyAsnAsn 779
      |||||||
Db 1828 GACAAATGCTCTTGATCTGATGCTGTGAAGACGTCTGTGGGTGTGTAAACGGGAATAAC 1887

QY 780 SerAlaCysThrIleHisArgGlyLeuTyrThrLysHisHisHisThrAsnGlnTyrTyr 799
      |||||||
Db 1888 TCAGCCTGCACGATTCACAGGGGTCTTACACCAAGCACCAACCAACCAAC---TATTAT 1944

QY 800 HisMetValThrIleProSerGlyAlaArgSerIleArgIleTyrGluMetAsnValSer 819
      |||||||
Db 1945 CACATGCTCACCAATTCCTTCTTGAGCCCGGAGATTCGCAATCTATGAATGAACGTCTCT 2004

QY 820 ThrSerTyrIleSerValArgAsnAlaLeuArgArgTyrTyrLeuAsnGlyHisTrpThr 839
      |||||||
Db 2005 ACCCTCTACATTTCTGTGCGCAATGCCCTCAGAAAGTACTACTGAATGGGCACTGGACC 2064

QY 840 ValAspTrpProGlyArgTyrLysPheSerGlyThrThrPheAspTyrArgArgSerTyr 859
      |||||||
Db 2065 GTGGACTGGCCCGCCGGTACAATTTCGGGCACTACTTTCGACTACAGACGGTCTTAT 2124

QY 860 AsnGluProGluAsnLeuIleAlaThrGlyProThrAsnGluThrLeuIleValGluLeu 879
      |||||||
Db 2125 AATGAGCCCGAAGACTTAATCGCTACTGAGCCAAACAGACACTGATTGTGAGCTG 2184

QY 880 LeuPheGlnGlyArgAsnProGlyValAlaTrpGluTyrSerMetProArgLeuGlyThr 899
      |||||||
Db 2185 CTGTTTCAGGGAGAAACCCGGGTGTGCTCGGAATACTCCATGCCCTCGTTGGGGACC 2244

QY 900 GlnLysGlnProProAlaGlnProSerTyrThrTrpAlaIleValArgSerGlnCysSer 919
      |||||||
Db 2245 GAGAAAGCAGCCCTCTGCCAGCCACGCTACACTGGGCCCATCGTGGCTCTGAGTGTCC 2304

QY 920 ValSerCysGlyGlyGlyArgCysLeuProValLeuLeuLeuGlnAlaCysGlnPro 939
      |||||||
Db 2305 GTGTCTGCGGAGGGGTAGGTGCTTCCAGTGTCTCTCTGGAGGCGACATGTCAACCT 2364

QY 940 SerAlaThrAlaTyrIleAlaLeuAlaPheLeuGlnSer 952
      |||||||
Db 2365 TCAGCCACTGCGTACATTGCACTGGCCTTCTTGAATCC 2403

RESULT 4
US-10-330-176-1
; Sequence 1, Application US/10330176
; Publication No. US20030228676A1
; GENERAL INFORMATION:
; APPLICANT: Agostino, Michael
; APPLICANT: DiBlasio, Elizabeth
; TITLE OF INVENTION: AGGRECANASE MOLECULES
; FILE REFERENCE: AM100884
; CURRENT APPLICATION NUMBER: US/10/330,176
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: 60/344,895
; PRIOR FILING DATE: 2001-12-31
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; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 3675
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-176-1

Alignment Scores:
Pred. No.: 0 Length: 3675
Score: 3993.50 Matches: 766
Percent Similarity: 78.36% Conservative: 16
Best Local Similarity: 76.75% Mismatches: 37
Query Match: 76.27% Indels: 181
DB: 17 Gaps: 10

US-09-981-151D-8 (1-952) x US-10-330-176-1 (1-3675)

QY 1 MetLysProArgAlaArgGlyTrpArgGlyLeuAlaAlaLeuTrpMetLeuLeuAlaGln 20
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Db 1 ATGAAGCCCCCGCGCGCGGATGGCGGGGCTTGGCGCGCTGTGATGCTGCGCGCAG 60

QY 21 ValAlaGluGlnValSerProGlyArgSerHisGlnArgGlyAsnArgGlySerGlyGln 40
      |||||||
Db 61 GTGGCCGAGCA----- 71

QY 41 LeuGluAlaSerProProArgLeuLeuSerArgGlyProArgArgLeuThrAlaMetSer 60
      |||||||
Db 71 ----- 71

QY 61 ProLeuPheSerAlaGlyThrCysValArgHisGlyThrArgSerGlySerAlaTrpGlu 80
      |||||||
Db 72 -----GGACCTGCGTGGCCATGGGACCCGCGAGCGGCGGCTGGAG 116

QY 81 ProGluArgProAlaSerSerSerThrArgGlyAlaAlaGlyLeuAspGly-LysGlyArg 100
      |||||||
Db 117 CCCGAGCGTCCCGCTCTCTCTCCACCCGCGAGCGGCGGCTGATGGAAAGGGC-- 174

QY 100 GAspMetAspGluAlaGlyAsnHisArgSerGlnGlnThrAsnThrGlyThrGluAsnGln 120
      |||||||
Db 174 ----- 174

QY 120 nThrLeuHisValLeuThrGlnTyrAspLeuValSerAlaTyrGluValAspHisArgGln 140
      |||||||
Db 175 -----GAATATGACCTGGTCTCTGCTTACGAGGTTGACCAAGGGG 215

QY 140 YAspTyrValSerHisGlnIleMetHisHisGlnArgArgArgAlaValAlaValSer 160
      |||||||
Db 216 CGATTACGTGTCATGAATCATGACCAACATCAGCGCGGAGAAAGACAGTGGCTGTC 275

QY 160 rGluValGlnSerLeuHisValArgLeuLysGlyProArgHisAspPheHisMetAspLe 180
      |||||||
Db 276 CGAGGTGAGTCTCTTCACTTCGGCTGAAAGGCCACAGCAGCACTTCCACATGGATCT 335

QY 180 uArgThrSerSerSerLeuValAlaProGlyPheIleValGlnThrLeuGlyLysThrGln 200
      |||||||
Db 336 GAGGACTTCCAGCAGCCTTAGTGGCTCTGCTTATTGTGCAGACGTTGGAAAGACAGG 395

QY 200 YThrLysSerValGlnThrLeuProProGluAspPheCysPheTyrGlnIlySerLeuArg 220
      |||||||
Db 396 CACTAAGTGTGTGACAGACTTAACGCCAGAGAACTTCTGTTCATCAAGGCTCTTTGGC 455

QY 220 gSerHisArgAsnSerProSerHisGlyGlyLysPheCysGluGlySerThrArgThrLe 240
      |||||||
Db 456 ATCACACAGAAACTCC---TCAGTGGCCCTTCAACCTGCAAGGCTGTGAGGCATGAT 512

QY 240 uLysLeuCysAsnSerGlnLysCysProArgAspSerValAspPheArgAlaAlaGlnCys 260
      |||||||
Db 513 ACGA-----ACAGAAGAGGAGATTAATTCTTAAGGCCACT 548

QY 260 sAlaGluHisAsnSerArgArgPheArgGlyArgHisTyrLysTrpLysProTyrThrGln 280
      |||||||
Db 549 TCCTTCACACCTCTCA-----TGAAA----- 570
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QY 280 nValGluAlaAspLeuCysLysLeuTyrCysIle-AlaGluGlyPheAspPhePhePheS 300
Db 571 -----CTCGGCAAG----- 580
QY 300 exLeuSerAsnLysValLysAspGlyThrProCysSerGluAspSerArgAsnValCysI 320
Db 581 --CTGCCCAAGGCACTCGCCATCCCAAGAGATCTACAAGAGATCCACAGAGCCCATGC 638
QY 320 leAspGlyIleCysGluLeuSerValIleSerThrSer-----AlaHis----- 334
Db 639 TCCT-GGGGCCAGTGAAGTCCCTGGTGAACCTCAAGGACATGGAGCTGGCACATCAACCC 697
QY 334 ----- 334
Db 698 TGCACAGCAGCAGCCTTCGCTGGGAGCTGCCACAAGCAGCATTTCTGTGAAGACGCA 757
QY 335 -----MetProGlnProProLysGluAspLeuPheIleLeuProAspGluTyrLys 352
Db 758 AGAATATACATGCCCCAGCCTCCCAAGAGAGACCTCTTCATCTTGCCAGATGAGTATAGT 817
QY 352 erCysLeuArgHisLysArgSerLeuLeuArgSerHisArgAsnGluGluLeuAsnValG 372
Db 818 CTGCTTACGGCATTAAGCGCTCTCTTGAGGTCCCATAGAAATGAAGAACTGAACGTGG 877
QY 372 luThrLeuValValValAspLysLysMetMetGlnAsnHisGluHisGluAsnIleThrT 392
Db 878 AGACCTTGTTGGTGGTGCAGCAAAAGATGATGCACAAACCATGGCCATGAAATATACCA 937
QY 392 hrTyrValIleuThrIleLeuAsnMetValSerAlaLeuPheLysAsp----- 407
Db 938 CCTACGTGCTCAGATACTCAACATGTATCTGCTTATTCAAAGATGGAACAATAGAG 997
QY 407 ----- 407
Db 998 GAAACATCAACATTGCAATTGTAGTCTGATTCTTCTAGAAGTGAACAGCCAGACTGG 1057
QY 408 -----GlyLeuM 410
Db 1058 TGATAAGTCAACGACGACCAACACCTTAAGTAGCTTCTGCCAGTGGCAGTCTGGATTGA 1117
QY 410 etGlyLysAspGlyThrArgHisAspHisAlaIleLeuLeuThrGlyLeuAspIleCys 430
Db 1118 TGGGGAAGATGGGAGCTCGTCAATGACCAAGCCATCTTACTGACTGCTGATATATGTT 1177
QY 430 erTrpLysAsnGluProCysAspThrLeuGlyPheAlaProIleSerGlyMetCysSerL 450
Db 1178 CTGGAAGAATGAGCCCTGTGTACACTTTGGGATTGGACCCCATTAAGTGAATGTGTAGTA 1237
QY 450 ysTyrArgSerCysThrIleAsnGluAspThrGlyLeuGlyLeuAlaPheThrIleAlaH 470
Db 1238 AATATCGCAGCTGCACGATTATGAAGATACAGTCTTGAGCTGGCTTCAACCATTGCCC 1297
QY 470 leGluSerGlyHisAsnPheGlyMetIleHisAspGlyGluGlyAsnMetCysLysLys 490
Db 1298 ATGAGTCTGGACACAACCTTTGGCATGATTCAATGAGAGAGGGAACATGTATAAAAGT 1357
QY 490 erGluGlyAsnIleMetSerProThrLeuAlaGlyArgAsnGlyValPheSerTrpSerP 510
Db 1358 CCGAGGGCAACATCATGTCCCTTACATTGGCAGGACGCAATGGAGTCTTCTCTGGTCA 1417
QY 510 roCysSerArgGlnTyrLeuHisLysPheLeuSerThrAlaGlnAlaIleCysLeuAla 530
Db 1418 CCTGCAGCCGCCAGTATCTACAAATTTCTAAGCACCCGCTCAAGCTATCTGCTTGCTG 1477
QY 530 spGlnProLysProValLysGluTyrLysTyrProGluLysLeuProGluLeuTyrA 550
Db 1478 ATCAGCCAAAGCCTGTGAAGGAAATCAAGTATCTGAGAAATTGCCAGAGAAATTATATG 1537
QY 550 spAlaAsnThrGlnCysLysTrpGlnPheGlyGluLysAlaLysLeuCysMetLeuAsp 570
Db 1538 ATGCAACACACAGTGCAGAGTGGCAGTTCCGAGAGAAAGCCAAAGCTCTGCAATGCTGACT 1597

QY 570 helysLysAspIleCysLysAlaLeuTrpCysHisArgIleGlyArgLysCysGluThrL 590
Db 1598 TTAAAAAGACATCTGTAAAGCCCTGTGGTGGCCATCGTATTTGGAAGAAATGTGAGACTA 1657
QY 590 ysPheMetProAlaAlaGluGlyThrIleCysGlyHisAspMetTrpCysArgGlyGlyG 610
Db 1658 AATTATGCAAGCAGCAGAGAGGACAAATTTGTGGCATGACATGTGTGGCGGAGAGAC 1717
QY 610 lncysValLysTyrGlyAspGluGlyProLysProThrHisGlyHisIleTrpSerAspTrpS 630
Db 1718 AGTGTGAATATATGTTATGAAGGCCCAAGCCACCATGGCCACTGTCGACTGCT 1777
QY 630 erSerTrpSerProCysSerArgThrCysGlyGlyValSerHisArgSerArgLeu 650
Db 1778 CTTCTTGTCCTCCATGCTCCAGACCTGGCGAGGGGAGTATCTCATAGAGTGCCTCT 1837
QY 650 ysThrAsnProLysProSerHisGlyGlyLysPheCysGluGlySerThrArgThrLeu 670
Db 1838 GCACCAACCCCAAGCCATCGCATGAGGGAAGTTCTGTGAAGGCTCCACTCGCACTTGA 1897
QY 670 ysLeuCysAsnSerGlnLysCysProArgAspSerValAspPheArgAlaAlaGlnCysA 690
Db 1898 AGCTCTGCAACAGTCAGAAATGTCCCGGAGACAGTGTGACTTCCGTGCTCAGTGTG 1957
QY 690 laGluHisAsnSerArgArgPheArgGlyArgHisTyrLysTrpLysProTyrThrGlnV 710
Db 1958 CCGAGCAACAACAGCAGACGATTCAGAGGGCGGCACCTACAAGTGAAGCCTTACACTCAAG 2017
QY 710 alGluAspGlnAspLeuCysLysLeuTyrCysIleAlaGluGlyPheAspPhePhePheS 730
Db 2018 TAGAAGATCAGGACTTATGCAAACTTACTGTATCGCAAGAGATTGATTCTCTTTT 2077
QY 730 erLeuSerAsnLysValLysAspGlyThrProCysSerGluAspSerArgAsnValCysI 750
Db 2078 CTTTGTCAATTAAGTCAAAAGATGGGACTCCATGCTCGAAGATAGCCGTAAATGTTGTA 2137
QY 750 leAspGlyIleCysGluArgValGlyCysAspAsnValLeuGlySerAspAlaValGluA 770
Db 2138 TAGATGGATATGTGAGAGAGTTGAGTGTGACAAATGTCTTGATCTGATGCTGTTGAAG 2197
QY 770 spValCysGlyValCysAsnGlyAsnAsnSerAlaCysThrIleHisArgGlyLeuTyrT 790
Db 2198 ACGTCTGGGGGTGTGTAAACGGGAATTACTCAGCCTGCACGATTCAAGGGGTCTCTACA 2257
QY 790 hrLysHisHisIleThrAsnGlnTyrThrHisMetValThrIleProSerGlyAlaArgS 810
Db 2258 CCAAGCACCAACACACCAACAGTATATACATGTCACCATTCCTCTGGAAGCCCGGA 2317
QY 810 erIleArgIleTyrGluMetAsnValSerThrSerTyrIleSerValArgAsnAlaLeuA 830
Db 2318 GTATCCGATCTATGAATGAACGTCTTACCTCCTACATTTCTGTGGCAATGCCCTCA 2377
QY 830 rgArgTyrTyrLeuAsnGlyHisTrpThrValAspTrpProGlyArgTyrLysPheSerG 850
Db 2378 GAAGGTACTACCTGAATGGGCACTGCACCGTGCAGTGGCCCGGTACAATTTTCGG 2437
QY 850 lyThrThrPheAspTyrArgArgSerTyrAsnGluProGluAsnLeuIleAlaThrGlyP 870
Db 2438 GCACTACTTTCGACTACAGACGCTCCTATATAGAGCCCGAAGACTTATCGCTACTGGAC 2497
QY 870 roThrAsnGluThrLeuIleValGluLeuLeuPheGlnGlyArgAsnProGlyValAlaIat 890
Db 2498 CAACCAACGAGACACTGATGTGTGAGTGTCTGTTCAAGGAAGAACCCGGGTGTGCT 2557
QY 890 rpGluTyrSerMetProArgLeuGlyThrGluLysGlnProProAlaGlnProSerTyrT 910
Db 2558 GGGAATACTCCATGCTCGCTTGGGAGCCGAGAGACAGCCCTGCCAGCCAGCTTACA 2617
QY 910 hrTrpAlaIleValArgSerGluCysSerValSerCysGlyGlyArg 926
Db 2618 CTTGGGCATCGTGCCTCTGAGTGTCTCGTGTCTGCGGAGGGGGACAG 2667

RESULT 5

US-10-275-107-16
; Sequence 16, Application US/10275107
; Publication No. US20040063107A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY D.
; APPLICANT: WHYTE, DAVID
; APPLICANT: SUDARSANAM, SUCHA
; APPLICANT: MANNING, GERARD
; APPLICANT: CAENEPEEL, SEAN R.
; APPLICANT: PAYNE, VILLA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1479
; CURRENT APPLICATION NUMBER: US/10/275,107
; PRIOR FILING DATE: 2003-11-03
; PRIOR APPLICATION NUMBER: PCT/US01/14431
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/201,879
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 3675
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-275-107-16

Alignment Scores:
Pred. No.: 0 Length: 3675
Score: 3993.50 Matches: 766
Percent Similarity: 78.36% Conservative: 16
Best Local Similarity: 76.75% Mismatches: 37
Query Match: 76.27% Indels: 181
DB: 18 Gaps: 10

US-09-981-151D-8 (1-952) x US-10-275-107-16 (1-3675)

QY 1 MellySPRoArglaaRgGlyTTPrArgGlyLeuAlaLeuTTPMetLeuAlaGln 20
DB 1 ATGAAGCCCCCGCGCGCGGATGGCGGGCTTGCGCGCGCTGTGATGCTGCGCGCAG 60
QY 21 ValAlaGluGlnValSerProGlyArgSerHisGlnArgGlyAsnArgGlySerGlyGln 40
DB 61 GTGCGCGAGCA----- 71
QY 41 LeuGluAlaSerProProArgLeuLeuSerArgGlyProArgArgLeuThrAlaMetSer 60
DB 71 ----- 71
QY 61 ProLeuPheSerAlaGlyThrCysValArgHisGlyThrArgSerGlySerAlaTTPGlu 80
DB 72 -----GGCACCTGCGTGGCCATGGAGACCGCGAGCGCGAGCGCTGGAG 116
QY 81 ProGluArgProAlaSerSerSerSerThrArgGlyAlaAlaGlyLeuAspGly-LysGlyArg 100
DB 117 CCCGAGCGTCCCGCGTCTCTCCACCGCGAGCGCGCGGCTGGATGMAAAGGC-- 174
QY 100 GAAPMetAspGluAlaGlyAsnHisArgSerGlnGlnThrAsnThrGlyThrGluAaGln 120
DB 174 ----- 174
QY 120 nThrLeuHisValLeuThrGlnTyrAspLeuValSerAlaTyrGluValAspHisArgGly 140
DB 175 -----GAATATGACCTGCTCTCTCTGCTTACGAGTTGACCAAGGGG 215
QY 140 YAspTyrValSerHisGluIleMetCnHisGlnArgArgArgArgAlaValAlaIse 160
DB 216 CGATTACGTGTCCCATGAATCATGACCATCAGCGCGGAGAGAGACAGTGGCGGTGTC 275
QY 160 rGluValGluSerLeuHisLeuArgLeuLysGlyProArgHisAspPheHisMetAspLe 180
DB 276 CGAGGTGAGTCTTTCACCTTCGGCTGAAGGCCCAAGCACGACGACTTCCACATGATCT 335
QY 180 uArgThrSerSerSerLeuValAlaProGlyPheIleValGlnThrLeuGlyLysThrGln 200

DB 336 GAGGACTTCCAGCAGCCTAGTGGCTCTGGCTTTATTGTGCAGACGTTGGGAAGACAGG 395
QY 200 YThrLysSerValGlnThrLeuProProGluAspPheCysPheTyrGlnGlySerLeuArg 220
DB 396 CACTAAGTCTGTGCAGACTTTACCGCAGAGGACTTGTGTTTCTATCAAGGCTCTTGGC 455
QY 220 gSerHisArgAsnSerProSerHisGlyGlyLysPheCysGluGlySerThrArgThrLe 240
DB 456 ATCACACAGAACTCC--TCAGTGGCCCTTTCACCTGCGCAAGGCTTGTGAGGCATGAT 512
QY 240 uLysLeuCysAsnSerGlnLysCysProArgAspSerValAspPheArgAlaAlaGlnCys 260
DB 513 AGCA-----ACAGAAAGAGCAGATTACTTCTTAAGGCCACT 548
QY 260 sAlaGluHisAsnSerArgArgPheArgGlyArgHisTyrIleSTrPlysProTyrThrGln 280
DB 549 TCCTTCACACCTCTCA-----TGAAA----- 570
QY 280 nValGluAlaAspLeuCysLysLeuTyrCysIle-AlaGluGlyPheAspPhePhePhe 300
DB 571 -----CTCGCAGAG----- 580
QY 300 erLeuSerAsnLysValLysAspGlyThrProCysSerGluAspSerArgAsnValCysI 320
DB 581 --CTGCCAAGCAGCTCGCCATCCACGCTACTGTACAAAGATCCACAGAGCCCATGC 638
QY 320 leAspGlyIleCysGluLeuSerValValSerThrSer-----AlaHis----- 334
DB 639 TCCT-GGGGCCAAGTGAAGTCTGTGACCTCAAGACATGGAGCTGCACATCAACCCC 697
QY 334 ----- 334
DB 698 TGCAACAGCAGCAGCTTCGCTGGAGCTGCCAACAAGCAGCATTTCTGTGAAGACGCA 757
QY 335 -----MetProGlnProProLysGluAspLeuPheIleLeuProAspGluTyrLys 352
DB 758 AGAATATACATGCCCCAGCCTCCCAAGAGACCTTTCATCTTGCAGATGATTAAGT 817
QY 352 erCysLeuArgHisLysArgSerLeuLeuArgSerHisArgAsnGluLysLeuAsnValG 372
DB 818 CTTCCTTACGGCATAAAGCGCTCTCTTGAGGTCCCATAGAATGAAGAACTGAACGTGG 877
QY 372 LuThrLeuValValValAspLysLysMetMetGlnAsnHisGlyHisGluAsnIleThrT 392
DB 878 AGACCTTGGTGTGTGCACAATAAGATGACAAAACCATGGCCATGAATAATATCACCA 937
QY 392 hrTyrValLeuThrIleLeuAsnMetValSerAlaLeuPheLysAsp----- 407
DB 938 CCTACGTGCTCAGATACTCAATGATGTATCTGCTTATTCAAAAGATGAACAATAGAG 997
QY 407 ----- 407
DB 998 GAAACATCAACATTGCAATTGTAAGTCTGATTTCTTAGAGATGAACAGCCAGACTGG 1057
QY 408 -----GlyLeuM 410
DB 1058 TGATAAGTCACCAAGCAGACCAACCTTAAGTAGCTTCTGCCAGTGGCAGTGGATTGA 1117
QY 410 etGlyLysAspGlyThrArgHisAspHisAlaIleLeuLeuThrGlyLysLeuAspIleCys 430
DB 1118 TGGGGAAGAATGGGACTCGTCAATGACCAAGCCATCTTACTGACTGCTGGATATATGTT 1177
QY 430 erTrpLysAsnGluProCysAspThrLeuGlyPheAlaProIleSerGlyMetCysSerL 450
DB 1178 CCTGGAAGAATGAGCCCTGTGACACTTTGGGATTTGCCACCAATAAGTGAATGTAGTA 1237
QY 450 YSTyrArgSerCysThrIleAsnGluAspThrGlyLysGlyLysLeuAlaPheThrIleAlaH 470
DB 1238 AATATCGACGTGCAAGATTAATGAAGATACAGGCTTGGACTGGCCTTCAACATTGGCC 1297
QY 470 iGluSerGlyHisAsnPheGlyMetIleHisAspGlyGluGlyAsnMetCysLysLys 490

Db 1298 ATGAGTCTGGACAACTTTGGCATGATTCAATGATGAGAGGAACATGTGTAAAAAGT 1357
QY 490 erglglYasnIleMetSerProthrLeuAlaGlyArgAsnGlyValPheSerTrpSerP 510
Db 1358 CCGAGGGCAACATCATGTCCCTTACATTTGGCAGAGCAGCAATGGAGTCTTCTGTGTAC 1417
QY 510 roCySerArgGlnTrpLeuHisPheLeuSerThrAlaGlnAlaIleCyLeuAlaA 530
Db 1418 CTTCAGCCCGCCAGTATCTACACAAATTTCTAAGCACCGCTCAAGCTATCTGCTTCTG 1477
QY 530 spGlnProLysProValLysGlnTrpLysTrpProGluLysLeuProGluLeuTyra 550
Db 1478 ATCAGCCAAAGCCTGTGAAGGAATACAAGTATCTGAGAAATTTGCCAGAGAAATTATATG 1537
QY 550 spAlaAsnThrGlnCySlyStrpGlnPheGlyGluLysAlaLysLeuCySmetLeuAsp 570
Db 1538 ATGCAAACACACAGTGCAGAGTGGAGTTCCGAGAGAAAGCCAGCTCTGCATGCTGACT 1597
QY 570 helYsLYsAspIleCySlysaAlaLeuTrpCySHisArgIleGlyArgLysCySgluThrL 590
Db 1598 TTTAAAAAGGACATCTGTAAAGCCCTGTGTGTCATCTGTATGGAAAGAAATGTAGACTA 1657
QY 590 ySPHemecProAlaAlaGluGlyThrIleCySglYHisAspMetTrpCySArgGlyGlyG 610
Db 1658 AATTATGCCAGACAGAGAGCACAATTTGTGGCATGACATGTGTGTCGGGGAGGAC 1717
QY 610 lncYsValLysTrpGlyAspGluGlyProLysProthrHisGlyHisTrpSerAspTrps 630
Db 1718 AGTGTGTGAATATGTGTATGAAGGCCCCAAAGCCCACTATGCCACTGTGTGACTGTGT 1777
QY 630 erSerTrpSerProCySserArgThrCySglYGlyValSerHisArgSeraArgLeuc 650
Db 1778 CTTCTTGTGTCCTCATGCTCCAGSACTGCGAGGGGAGTATCTCATAGAGTGCCTCT 1837
QY 650 ySThrAsnProLysProSerHisGlyGlyLysPheCySgluGlySerThrArgThrLeuL 670
Db 1838 GCACCAACCCCAAGCCATCGCATGAGGAGGAAAGTTCTGTAGAGGCTCCACTCGCACTCTGA 1897
QY 670 ySLeuCySAsnSerGlnLysCySProArgAspSerValAspPheArgAlaAlaGlnCysA 690
Db 1898 AGCTCTGCMAACAGTCAGAAATGTCCCGGAGCAGTGTGACTTCCGTGCTGCTCAGTGTG 1957
QY 690 laGluHisAsnSerArgArgPheArgGlyArgHisTrpLysTrpLysProTrpThrGlnV 710
Db 1958 CCGAGCACCAACAGCAGACGATTCAGAGGCGGCACTACAAAGTGAAGCCTTCACTCAAG 2017
QY 710 aIGluAspGlnAspLeuCySlyLeuTrpCySleAlaGluGlyPheAspPhePhePheS 730
Db 2018 TAGAAGATCAGACTTATGCAAACTCTACTGTATCGCAGAAAGATTGATTCTTCTTTT 2077
QY 730 erLeuSerAsnLysValLysAspGlyThrProCySserGluAspSerArgAsnValCysI 750
Db 2078 CTTTGTCAAAATAAGTCMAAGATGGGACTCCATGCTCGAGAGTAGCCGTATGTTTGTGA 2137
QY 750 leAspGlyIleCySgluArgValGlyCySAspAsnValLeuGlySerAspAlaValGluA 770
Db 2138 TAGATGGATATGTAGAGAGATTGATGTGACAAATGCTCTTGATCTGATGCTGTTGAAG 2197
QY 770 spValCySglYValCySAsnGlyAsnAsnSeraIaCySThrIleHisArgGlyLeuTyrt 790
Db 2198 ACGTCTGTGGGTGTGTAAACGGGAATAACTGACCTGCACGATTCACAGGGGTCTTACA 2257
QY 790 hrLYsHisHisThrAsnGlnTrpTrpHisMetValThrIleProSerGlyAlaArgS 810
Db 2258 CCAAGCACCAACACCAACCAAGTATTATACATGTGTACCAATTCCTTCGAGCCCGGA 2317
QY 810 erIleArgIleTyrgIuMeAsnValSerThrSerTrpIleSerValArgAsnAlaLeuA 830
Db 2318 GTATCCGCATCTATGAATAGAAAGTCTCTACCTCCTACATTTCTGTGCGCAATGCCCTCA 2377
QY 830 rgArgTrpTrpLeuAsnGlyHisTrpThrValAspTrpProGlyArgTrpLysPheSerG 850
Db 2378 GAAAGTACTACTGAATGGGCACTGGACCGGTGGAAGTGGCCCGGTACAAATTTTCGG 2437

QY 850 lYThrThrPheAspTrpArgArgSerTrpAsnGluProGluAsnLeuIleAlaThrGlyP 870
Db 2438 GCACTACTTTCGACTACAGACGGTCTCTAATAAGAGCCCGAGAACTTAATGCTACTGAC 2497
QY 870 roThrAsnGluThrLeuIleValGluLeuLeuPheGlnGlyArgAsnProGlyValAlaT 890
Db 2498 CAACCAAGACAGACACTGATTGTGTGAGCTGCTGTTTCAGAGGAAGAAGAACCCGGGTGCT 2557
QY 890 rpGluTrpSerMetProArgLeuGlyThrGluLysGlnProProAlaGlnProSerTrpT 910
Db 2558 GGAATACTCCATGCTCGCTTGGGGACGAGAGACAGCCCTGCCAGCCCACTACA 2617
QY 910 hrTrpAlaIleValArgSerGluCySserValSerCySglYGlyArg 926
Db 2618 CTTGGCCATCGTGCCTCTGAGTGTCTCCGTCTGCGGAGGGGACAG 2667

RESULT 6
US-10-217-774-3
; Sequence 3, Application US/10217774
; Publication No. US20020193583A1
; GENERAL INFORMATION:
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Hilbun, Erin
; TITLE OF INVENTION: No. US20020193583A1e1 Human Proteases and Polynucleotides Encoding
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0219-USA
; CURRENT APPLICATION NUMBER: US/10/217,774
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US/09/930,872
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,852
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3675
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-217-774-3

Alignment Scores:
Pred. No.: 0 Length: 3675
Score: 3981.50 Matches: 764
Percent Similarity: 78.26% Conservative: 17
Best Local Similarity: 76.55% Mismatches: 38
Query Match: 76.04% Indels: 181
DB: 13 Gaps: 10

US-09-981-151D-8 (1-952) x US-10-217-774-3 (1-3675)

QY 1 MetLysProAlaArgGlyTrpArgGlyLeuAlaLeuTrpMetLeuLeuAlaGln 20
Db 1 ATGAAGCCCCCGCGCGGATGGCGGGCTTGCGCGCTGTGATGCTGCGCGCAG 60
QY 21 ValAlaGluGlnValSerProGlyArgSerHisGlnArgGlyAsnArgGlySerGlyGln 40
Db 61 GTGGCCGAGCA----- 71
QY 41 LeuGluAlaSerProArgLeuLeuSerArgGlyProArgArgLeuThrAlaMetSer 60
Db 71 ----- 71
QY 61 ProLeuPheSerAlaGlyThrCySValArgHisGlyThrArgSerGlySeraIaTrpGlu 80
Db 72 -----GGCACCTGCGTGGCCATGGGACCCGAGCGGACGCGCTGGAG 116
QY 81 ProGluArgProAlaSerSerSerThrArgGlyAlaAlaGlyLeuAspGlyLysGlyAr 100
Db 117 CCGGAGCGTCCCGCGTCTCTCCACCCGCGGAGCGGCGGGCTGATGAAAAAGGC-- 174
QY 100 gAspMetAspGluAlaGlyAsnHisArgSerGlnGlnThrAsnThrGlyThrGluAsnGln 120

Db 174 ----- 174
QY 120 nThrLeuHISValLeuThrglnTyraSPLeuValSerAlaTyrgluValAspHisArgG1 140
Db 175 -----GAATATGACCTGCTCTGCTGCTACGAGGTTGACCAAGGG 215
QY 140 yAspTyrValSerHisgluIleMetHisHisgluNArgArgArgArgAlaValAlaValSe 160
Db 216 CGATTACGTGTCCCATGAATATCATGACCATCAGCGCGGAGAGAGACAGTGGCGGTGC 275
QY 160 rgluValgluSerLeuHisleuArgleuLysglYProArgHisAspPheHisMetAspLe 180
Db 276 CGAGGTTGAGTCTTCACTTCAGCTCGGCTGAAGGCTCCAGCAGCAGCTTCACGTGATCT 335
QY 180 uArgThrSerSerSerLeuValAlaProglYpHeIleValgluNThrLeuGlYLeThrG1 200
Db 336 GAGAGCTTCCAGCAGCCTAGTGGCTCCTGGCTTTATGTGACAGACGTTGGAAAGACAG 395
QY 200 yThrLysSerValgluNThrLeuProProgluAspPheCysPheTyrgluNglYSerLeuAr 220
Db 396 CACTAAGTCTGTGACAGACTTACC GCCAGAGGACTTCTGTTCATCAAGGCTCTTGGCG 455
QY 220 gSerHisArgAsnSerProSerHisglYglYLySPheCysgluGlYSerThrArgThrLe 240
Db 456 ATCAACACAGAAACTCC--TCAgTgCCCTTTCAACCTGCCCAAGGCTTGTCAAGGCAATGAT 512
QY 240 ulYsLeuCybaSnSerGlnLysCySProArgAspSerValAspPheArgAlaAlaGlnCy 260
Db 513 ACCG-----ACAGAGAGGCGAGATTACTTCTTAAGGCCACT 548
QY 260 salagluHisAsnSerArgArgPheArgglYArgHisTyrgTyrgLysProTyrgThrG1 280
Db 549 TCCTTCACACCTCTCA-----TGGAAA----- 570
QY 280 nValgluAlaAspLeuCySylsLeuTyrgCysile-AlagluGlYpHeAspPhePheS 300
Db 571 -----CTGGCGAGAG----- 580
QY 300 erLeuSerAsnLysValLysAspglYThrProCySserGluAspSerArgAsnValCysI 320
Db 581 --CTGCCCAAGGCACTCGCCATCCCACTGACTGTACAAGAGATCCAAGAGCCCATGC 638
QY 320 leAspglYIleCySgluLeuSerValAlSerThrser-----AlaHis----- 334
Db 639 TCCT-GGGGCCAGTGAAGGTCTGTGACCTCAAGGACATGGAGCTGGACATCAACCC 697
QY 334 ----- 334
Db 698 TGCAACAGCAGCGACCTTGGCTGGACTGCCACAAAGCAGCATTTCTGTGAAGACGCA 757
QY 335 -----MetProGlnProProIySgluAspLeuPheIleLeuProAspgluTyrgLys 352
Db 758 AGAATAATACATGCCCAAGCCTCCCAAGAAAGACCTTTCATCTTGCAGATGAGTAAAGT 817
QY 352 erCySleuArgHisLysArgSerLeuLeuArgSerHisArgAsngluGlYLeuAsnValG 372
Db 818 CTTCCTTACGGCATTAAGCGCTCTTCTGTAGGCTCCCATAGAAATGAAGAACTGAACGTGG 877
QY 372 luThrLeuValValValAspLysLysMetMetGlnAsnHisglYHisgluAsnIleThrt 392
Db 878 AGACCTTGGTGTGTGACAAAGATGATGCAAAACCATGGCCATGAAATATACCA 937
QY 392 hrTyrgValLeuThrIleLeuAsnMetValSerAlaLeuPheLysAsp----- 407
Db 938 CCTACGTGCTCAGCTACTCAACATGTGTATCTGTTATTCAAGATGGAACAAATAGGAG 997
QY 407 ----- 407
Db 998 GAAACATCAACATTGCAATTGTAGTCTGATTCTTCTAGAGATGAACAGCAGGACTGG 1057
QY 408 -----glyLeuM 410
Db 1058 TGATAAGTCAACACGACAGACACACTTAAGTAGCTTCTGCCAGTGGCAGTCTGGATTGA 1117

QY 410 ecGluLysAspglYThrArgHisAspHisAlaIleLeuLeuThrglYLeuAspIleCysS 430
Db 1118 TGGGGAAGATGGGAACTCGTCAATGACCAGCCCATCTTACTGACTGCTGTGATATATGTT 1177
QY 430 erTrpLysAsngluProCySAspThrLeuGlYpHeAlaProIleSerGlyMetCysSerL 450
Db 1178 CTTGGAAGAAATGAGCCCTGTGACACTTGGGATTTGCACCCATTAAGTGAATGTAGTA 1237
QY 450 ySTyrArgSerCysThrIleAsngluAspThrnglYLeuGlYLeuAlaPheThrIleAlaH 470
Db 1238 AATATCGAGCTGCAAGATTAAATGAAGATACAGGCTTGGACTGGCTTCACCATTTGCC 1297
QY 470 isgluSerGluHisAsnPheglYMetIleHisAspglYgluGlYAsnMetCySlysLys 490
Db 1298 ATGAGTCTGACACAACCTTGGCATGATTGATGATGAGAGGGAACATGTAAAGT 1357
QY 490 ergluGlYAsnIleMetSerProThrLeuAlagluYArgAsnglYValPheSerTrpSerP 510
Db 1358 CCGAGGCAACATCATGTCCCTTACATTGGCAGAGACGCAATGGAAGTCTTCCTGCTCAC 1417
QY 510 roCySserArgGlnTyrgLeuHisLysPheLeuSerThrAlaGlnAlaIleCySleuAla 530
Db 1418 CTTGACAGCCGCCAGTATCTACAAATTTCTAAGCACCCGCTCAAGCTATCTGCTTGTCTG 1477
QY 530 spGlnProLysProValLysgluTyrgTyrgTyrgProgluLysLeuProglYgluLeuTyra 550
Db 1478 ATCAGCCAAAGCCTGTGAAGGAATACAAAGTATCTTGAGAAATTTGCCAGAGAAATTATATG 1537
QY 550 spAlaAsnThrGlnCySylsTyrgLysPheglYgluLysAlaLysLeuCySmetLeuAsp 570
Db 1538 ATGCAACACACAGTGAAGTGGCAGTTCGGAGAGAAAGCCAACTCTGCACTGCTGAGCT 1597
QY 570 helYsLysAspIleCySylsAlaLeuTyrgCysHisArgIleglYArgLysCySgluThrl 590
Db 1598 TTAATAAGACATCTGTAAAGCCCTGTGTGTCATCGTATTTGAAGAAATGTGAGACTA 1657
QY 590 ySPheMetProAlaAlagluGlYThrIleCySgluYHisAspMetTrpCySArgglYglYg 610
Db 1658 AATTATGCCAGCAGCAGAGGCAACAATTGTGGCATGACATGTGTGCCGGGAGAGAC 1717
QY 610 lncYsValLysTyrglYAspgluGlYProLysProThrHisglYHisTrpSerAspTrps 630
Db 1718 AGTGTGTGAATATGTGTATGAAGGCCCAAGCCCACTGAGGCCACTGTGTGGACTGTT 1777
QY 630 erSerTrpSerProCySserArgThrCySglYglYglYValSerHisArgSerArgLeuC 650
Db 1778 CTTCCTGTGTCCTCATGCTCCAGAACCTGCGGAGGGGAGTATCTCATAGAGTGCCTCT 1837
QY 650 ySThrAsnProLysProSerHisglYglYLysPheCySgluGlYSerThrArgThrLeuL 670
Db 1838 GCACCAACCCCAAGCCATCGCATGGAAGGAAAGTTCTGTAGGGCTCCACTCGCACTCTGA 1897
QY 670 ySleuCySAsnSerGlnLysCySProArgAspSerValAspPheArgAlaAlaGlnCysA 690
Db 1898 AGCTCTGCAACAGTCAAGAAATGTCCCGGACAGTGTGACTTCCGTGCTCACTGTGTG 1957
QY 690 lagluHisAsnSerArgArgPheArgglYArgHisTyrgLysTrpLysProTyrgThrGlnv 710
Db 1958 CCGAGCACACACAGACGAGATTCAAGAGGCGGCACTACAAGTGAAGCCTTACACTCAAG 2017
QY 710 algluAspGlnAspLeuCySylsLeuTyrgCysIleAlagluGlYpHeAspPhePheS 730
Db 2018 TAGAAGATCAGGACTTATGCAAACTCTACTGTATCGCAGAAAGATTGATTCTTCTTTT 2077
QY 730 erLeuSerAsnLysValLysAspglYThrProCySserGluAspSerArgAsnValCysI 750
Db 2078 CTTTGTCAAAATAAAGTCAAGATGGGACTTCATGCTCGAGAGATAGCCGTAAATGTTGTA 2137
QY 750 leAspglYIleCySgluArgValglYCybaSPAsnValLeuGlYSerAspAlaValgluA 770
Db 2138 TAGATGGGATATGTGAGAGAGTTGGATGTGTGACAAATGTCTTGGAATCTGATGCTGTGAAG 2197

QY 770 spValCysGlyValCysAsnGlyAsnAsnSerAlaCysThrIleHisArgGlyLeuTyrT 790
DB 2198 ACCTCTGTGGGGTGTGTAAACGGGAATTAAGTCACTGACGATTCACAGGGGTCTCTACA 2257
QY 790 hrIysHisHisHisThrAsnGlnTyrHisMetValThrIleProSerGlyAlaArgS 810
DB 2258 CCAAGCACCAACCAACCAAGTATATACATGATGTCACCATTCCTTGAGCCCGGA 2317
QY 810 erIleArgIleTyrGluMetAsnValSerThrSerTyrIleSerValArgAsnAlaLeu 830
DB 2318 GTATCCGCATCTATGAATGAACGCTCTCTACCTCTACATTTCTGTGCGAATGCCCTCA 2377
QY 830 rGArgTyrTyrLeuAsnGlyHisIleTrpThrValAspTrpProGlyArgTyrIleSbSerg 850
DB 2378 GAAGGTACTACCTGAATGGGACATGGACCGTGGACCTGGCCCGGTACAAATTTTCGG 2437
QY 850 lYThrThrPheAspTyrArgArgSerTyrAsnGluProGluAsnLeuIleAlaThrGlyP 870
DB 2438 GCACTACTTTCGACTACAGACGGTCTTATATGAGCCCGAAGACTTAATCGTACTGGAC 2497
QY 870 roThrAsnGluThrLeuIleValGluLeuLeuPheGlnGlyArgAsnProGlyValAlaIat 890
DB 2498 CAACCAACGAGACACTGATTGTGAGCTGCTGTTCAGGAGGAACCCGGGTGTGCCT 2557
QY 890 rPGluTyrSerMetProArgLeuGlyThrGluYsgInProProAlaGlnProSerTyrT 910
DB 2558 GGGAAATACTCCATGCTCGCTTGGGGAGCCGAGAGACAGCCCTGCCCCAGCCCACTACA 2617
QY 910 hrTrpAlaIleValArgSerGluCysSerValSerCysGlyGlyArg 926
DB 2618 CTTGGGCCATCGTCGCTCTGAGTGTCTCGTGTCTGCGAGGGGGAGACAG 2667

RESULT 7
US-10-296-616-1
; Sequence 1, Application US/10296616
; Publication No. US20030129658A1
; GENERAL INFORMATION:
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: No. US20030129658A1el protease
; FILE REFERENCE: Y0132PCT-664
; CURRENT APPLICATION NUMBER: US/10/296,616
; PRIOR FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: JP 2000-393372
; PRIOR FILING DATE: 2000-12-25
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 1
; LENGTH: 3675
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3675)
US-10-296-616-1

Alignment Scores:
Pred. No.: 0 Length: 3675
Score: 3981.50 Matches: 764
Percent Similarity: 78.26% Conservative: 17
Best Local Similarity: 76.55% Mismatches: 38
Query Match: 76.04% Indels: 181
DB: 15 Gaps: 10

US-09-981-151D-8 (1-952) x US-10-296-616-1 (1-3675)

QY 1 MetLysProArgAlaArgGlyTrpArgGlyLeuAlaAlaLeuTrpMetLeuLeuAlaGln 20
DB 1 ATGAAGCCCCCGCGCGCGGATGGCGGCTTGGCGCGCTGTGATGCTGTGGCGCAG 60
QY 21 ValAlaGluGlnValSerProGlyArgSerHisGlnArgGlyAsnArgGlySerGlyGln 40
DB 61 GTGGCCGAGCA----- 71
QY 41 LeuGluAlaSerProProArgLeuLeuSerArgGlyProArgArgLeuThrAlaMetSer 60

DB 71 ----- 71
QY 61 ProLeuPheSerAlaGlyThrCysValArgHisGlyThrArgSerGlySerAlaTrpGlu 80
DB 72 -----GGACCTGCGTGGCCATGGGACCCGACGGCGCCTGGAG 116
QY 81 ProGluArgProAlaSerSerSerThrArgGlyAlaAlaGlyLeuAspGly-LysGlyAr 100
DB 117 CCCGAGCGTCCCGCGTCTCTCTCCACCCCGGAGCGCGGCTGGATGGAAGGGC-- 174
QY 100 GAspMetAspGluAlaGlyAsnHisArgSerGlnGlnThrAsnThrGlyThrGluAsnG 120
DB 174 ----- 174
QY 120 nThrLeuHisValLeuThrGlnTyrAspLeuValSerAlaTyrGluValAspHisArgG 140
DB 175 -----GAATATGACCTGCTCTGCTTACGAGGTGACACAGGGG 215
QY 140 YAspTyrValSerHisGluIleMetHisHisGlnArgArgArgAlaValAlaValSe 160
DB 216 CGATTACGTGTCCCATGAATCATGACCATCAGCGCGGAGAGAGAGAGAGAGAGAGAG 275
QY 160 rGluValGluSerLeuHisLeuArgLeuGlyGlyProArgHisAspPheHisMetAspLe 180
DB 276 CGAGGTGAGTCTCTTCACTTTCGGCTGAAAGGCTCCAGGACAGACTTCCACGTGATCT 335
QY 180 uArgThrSerSerSerLeuValAlaProGlyPheIleValGlnThrLeuGlyLysThrG 200
DB 336 GAGGACTTCCACAGAGCTAGTGGCTCTGAGCTTATTTGTGCAGACGTTGGGAAAGACAG 395
QY 200 YThrLysSerValGlnThrLeuProProGluAspPheCysPheTyrGlnGlySerLeuAr 220
DB 396 CACTAAGTCTGTGACAGACTTACCGCCAGAGAGACTTCTGTTCATCAAGCTCTTTGCC 455
QY 220 gSerHisArgAsnSerProSerHisGlyGlyLysPheCysGlyGlySerThrArgThrIle 240
DB 456 ATCACACAGAAACTCC---TCAGTGGCCCTTCAACCTGCCAAGGCTGTTCAGGCATGAT 512
QY 240 uLysLeuCysAsnSerGlnLysCysProArgAspSerValAspPheArgAlaAlaGlnCy 260
DB 513 ACGA-----ACAGAAAGAGCAGATTACTTCTTAAGGCCACT 548
QY 260 sAlaGluHisAsnSerArgArgPheArgGlyArgHisTyrLysTrpLysProTyrThrG 280
DB 549 TCCTTCACACCTCTCA-----TGAAA----- 570
QY 280 nValGluAlaAspLeuCysLysLeuTyrCysIle-AlaGluGlyPheAspPhePheS 300
DB 571 -----CTGGCAGAG----- 580
QY 300 erLeuSerAsnLysValLysAspGlyThrProCysSerGluAspSerArgAsnValCysI 320
DB 581 --CTGCCAAGGCAGCTCGCCATCCACGTACTGTACAGAGATCCACAGAGCCCATGCG 638
QY 320 leAspGlyIleCysGluLeuSerValSerThrSer-----AlaHis----- 334
DB 639 TCCT-GGGGCCAGTGAGGTCTGTGACCTCAAGACATGGAGCTGGACATCAACCCC 697
QY 334 ----- 334
DB 698 TGCACAGACGACCTTCGCTGGAGTGCACAAAGCAGCATTTCTGTGAAGACGCA 757
QY 335 -----MetProGlnProProLysGluAspLeuPheIleLeuProAspGluTyrLysS 352
DB 758 AGAATACATGCCCCCAGCTCCCAAGGAAGACCTTTCATCTTGCCAGATGAGTATAGT 817
QY 352 erCysLeuArgHisLysArgSerLeuLeuArgSerHisArgAsnGluLeuAsnValG 372
DB 818 CTTGCTTACGGCATAGCGCTCTCTTGAGGTCCCATAGAAATGAAGAACTGAACGTGG 877
QY 372 luthrLeuValValValAspLysLysMetMetGlnAsnHisGlyHisGluAsnIleThrT 392

Db 878 AGACCTTGTTGTTGCGACAAAAAGATGATGCAAAACCATGGCCATGAAATATACCA 937
QY 392 hrrYrValleuthrileuAsnmetValserAlaleuPheLysAsp----- 407
Db 938 CCTACGTGCTACGATACTCAACATGGTATCTGCTTATTCAAGATGGAACAATAGAG 997
QY 407 ----- 407
Db 998 GAAACATCAACATTCGAATTGTAGTCTGATTCTTGAAGATGAACAGCAGACTGG 1057
QY 408 -----glyLeuM 410
Db 1058 TGATAAGTCACCAAGCAGACCAACACTTAAGTCTTCCAGTGGCAGTCTGGATTGA 1117
QY 410 eeglyLysAspGlyThrArgHisAspHisAlaleuLeuThrGlyLeuAspIleCys 430
Db 1118 TGGGGAAGAATGGGACTCGTCATGACACGCCCATCTTACTGACTGGTCTGGATATAGTT 1177
QY 430 eerrPLysAsnGluProCysAspThrLeuGlyPheAlaProIleserGlymetCysSerL 450
Db 1178 CCTGGAAGAATGAGCCCTGTGACACTTTGGGATTGGCAACCATAGTGAATGTGTAGTA 1237
QY 450 yerrYrArgSerCysThrIleAsnGluAspThrGlyLeuGlyLeuAlaPheThrIleAlaH 470
Db 1238 AATATCGCAGCTGCACGATTAATGAAGATACAGGTCCTTGACTGGCCTTCAACCATGGCC 1297
QY 470 legLysSerGlyHisAsnPheGlymetIleHisAspGlyGlyLysAsnmetCysLysLys 490
Db 1298 ATGAGTCTGGACACAACTTTGGCATGATTCTATGATGAGAAGGGAACATGTGTAAAGT 1357
QY 490 eergLysGlyAsnIlemetSerProThrLeuAlaGlyArgAsnGlyValPheSerTrpSerP 510
Db 1358 CCGAGGGCAACATCATGTCCCTCATCTGGCAGGACCAATGAGAGTCTTCTCCTGCTCAC 1417
QY 510 roCySerArgGlnTyrrLeuHisLysPheLeuSerThrAlaGlnAlaIleCysLeuAlaA 530
Db 1418 CCTGCAAGCCGCCAGATATCTACAACAATTTCTAAGCACCGCTCAAGCTATCTGCTTGTG 1477
QY 530 epgLInProLysProValLysGlyUtyrLysTyrrProGlyLysLeuProGlyGlyLeuTyra 550
Db 1478 ATCAGCCAAAGCCTGTGAAGGAATACAGTATCTGAGAAATTTGCCAGGAATTAATATG 1537
QY 550 eprAlaAsnThrGlnCysLysTyrrGlnPheGlyGlyLysAlaLysLeuCysmetLeuAsp 570
Db 1538 ATGCCAAACACACAGTGCAGAGTGGCAGTTCCGAGAGAAAGCCCAAGCTCTGCATGCTGGA 1597
QY 570 helYsLysAspIleCysLysAlaLeuTrpCysHisArgIleGlyArgLysCysGluThrL 590
Db 1598 TTAATAAGACATCTGTAAAGCCCTGTGTGTCATCTGTAATTGAAAGAAATGTGAGACTA 1657
QY 590 yspPheMetProAlaAlaGluGlyThrIleCysGlyHisAspMetTrpCysArgGlyGlyG 610
Db 1658 AATTATATGCCAGCAGACAGAGGCACAATTTGTGGCATGATGTGTGCCGGGAGGAC 1717
QY 610 lncYsValLysTyrrGlyAspGlyLysProLysProThrHisGlyHisIleTrpSerAspTrpS 630
Db 1718 AGTGTGTGAATATGTGTATGAAGGCCCAAGGCCCAATGAGCCATGAGCTGTGGAAGTGTG 1777
QY 630 exSerTrpSerProCysSerArgThrCysGlyGlyValSerHisArgSerArgLeu 650
Db 1778 CTTCCTTGGTCCCATGTCTCCAGGACTTGGAGGGGAGTATCTCATAGAGTCCCTCT 1837
QY 650 yerrThrAsnProLysProSerHisGlyGlyLysPheCysGlyLysSerThrArgThrLeuL 670
Db 1838 GCACCAACCCCAAGCCATCGCATGGAGGGAAGTTGTGTGAGGGCTCCACTCGCACTCTGA 1897
QY 670 yLeuCyAsnSerGlnLysCysProArgAspSerValAspPheArgAlaIleGlnCysA 690
Db 1898 AGCTCTGCACAAGTCAGAATATGTCCTGGGACAGTGTGACTTCCGTGCTGCTGAGTGTG 1957
QY 690 laGluHisAsnSerArgArgPheArgGlyArgHisIleTyrrLysTrpLysProTyrrThrGln 710
Db 1958 CCGAGCACAAACAGACAGATTCAGAGGGCGGCACTAACAAGTGGAAGCCTTACACTCAAG 2017

QY 710 aIGluAspGlnAspLeuCyLysLysLeuTyrrCysIleAlaGluGlyPheAspPhePheS 730
Db 2018 TAGAAGATCAGGACTTATGCAAACTCTACTGTATTCGAGAGGATTTGATTTCTTTT 2077
QY 730 erLeuSerAsnLysValLysAspGlyThrProCysSerGlyLysAspSerArgAsnValCysI 750
Db 2078 CTTTGTCAAAATAAAGTCAAGATGGGACTCCATGCTCGAGAGATAGCCGTATGTTGTA 2137
QY 750 leAspGlyIleCysGlyLysArgValGlyCysAspAsnValLeuGlySerAspAlaValGlu 770
Db 2138 TAGATGGATATGTAGAGAGATTGGATGTGACAAATGTCCTTGGAATCTGATGCTGTGAAG 2197
QY 770 eprValCysGlyValCysAsnGlyAsnAsnSerAlaCysThrIleHisArgGlyLeuTyrr 790
Db 2198 AGTCTGTGGGTGTGTAAACGGAATAACTCAGCTCGACGATTCACAGGGGTCTTACA 2257
QY 790 hrrLysHisHisIleThrAsnGlnTyrrHisMetValThrIleProSerGlyAlaArgS 810
Db 2258 CCAAGCACACACACCAACCAAGTATTATACATGATGTCACCAATTCCTTGAGCCCGGA 2317
QY 810 erIleArgIleTyrrGlyLysLeuAsnValSerHisSerTyrrIleSerValArgAsnAlaLeu 830
Db 2318 GTATCCGATCTATGAATGAAGTCTCTACTCTTCAATTTCTGTGCGCAATGCCCCCTCA 2377
QY 830 rgarGlyrrTyrrLeuAsnGlyHisIleTrpThrValAspTrpProGlyArgTyrrLysPheSerG 850
Db 2378 GAAGTACTACTCGAATGGGCACTGGACCGTGACTGGCCCGGCGGTACAAATTTTTCGG 2437
QY 850 lyThrThrPheAspTyrrArgArgSerTyrrAsnGluProGlyLysLeuIleAlaThrGlyP 870
Db 2438 GCACTACTTTCGACTACAGACGGTCTTATATGAGCCCGAAGACTTAATCGTACTGAGC 2497
QY 870 roThrAsnGluThrLeuIleValGlyLeuLeuPheGlnGlyArgAsnProGlyValAlaIat 890
Db 2498 CAACCAACGAGACACTGATGTGGAGCTGCTGTTCAGAGGAAGAACCCGGGTGTGCCCT 2557
QY 890 rpgLutyrrSermetProArgLeuGlyThrGlyLysGlnProProAlaGlnProSerTyrrT 910
Db 2558 GGAATACTCCATGCTCGCTTGGGGAGCCGGAAGCAGCCCCCTGCCCCAGCCCACTACA 2617
QY 910 hrrTrpAlaIleValArgSerGluCysSerValSerCysGlyGlyArg 926
Db 2618 CTTGGGCCATCGTGGCTGTGAGTGTCTCGGTCTCGGAGGGGGAGACAG 2667

RESULT 8
US-10-804-457-3
; Sequence 3, Application US/10804457
; Publication No. US20050065334A1
; GENERAL INFORMATION:
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Hilbun, Erin
; TITLE OF INVENTION: Novel Human Proteases and Polynucleotides Encoding the
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0219-USA
; CURRENT APPLICATION NUMBER: US/10/804,457
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US/09/930,872
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,852
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3675
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-804-457-3
Alignment Scores: 0 Length: 3675
Pred. No.: 0

Score: 3981.50 Matches: 764
Percent Similarity: 78.26% Conservative: 17
Best Local Similarity: 76.55% Mismatches: 38
Query Match: 76.04% Indels: 181
DB: 21 Gaps: 10

US-09-981-151D-8 (1-952) x US-10-804-457-3 (1-3675)

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QY      1 MetLysProArgAlaArgGlyThrPArgGlyLeuAlaAlaLeuTrpMetLeuLeuAlaGln 20
DB      1 ATGAAGCCCCCGCGCGCGGATGGCGGGCTTGCGCGCGCTGTGGATGCTGTGGCGCAG 60
QY      21 ValAlaGluGlnValSerProGlyArgSerHisGlnArgGlyAsnArgGlySerGlyGln 40
DB      61 GTGGCCGAGCA----- 71
QY      41 LeuGluAlaSerProProArgLeuLeuSerArgGlyProArgArgLeuThrAlaMetSer 60
DB      71 ----- 71
QY      61 ProLeuPheSerAlaGlyThrCysValArgHisGlyThrArgSerGlySerAlaTrpGlu 80
DB      72 -----GGCACCTGCGTGGCCATGGGACCCGCAAGCGGACGCGCTGGAG 116
QY      81 ProGluArgProAlaSerSerSerThrArgGlyAlaAlaGlyLeuAspGly-LysGlyArg 100
DB      117 CCCGAGCGTCCCGCGCTCCTCTCCACCCGCGGAGCGCGCGGCTGGATGMAAAGGCG-- 174
QY      100 GAspMetAspGluAlaGlyAsnHisArgSerGlnGlnThrAsnThrGlyThrGluAsnGln 120
DB      174 ----- 174
QY      120 nThrLeuHisValLeuThrGlnTyArgPLeuValSerAlaTyArgLysValAspHisArgGln 140
DB      175 -----GAATATGACCTGGTCTCTGCTACGAGGTTGACCAAGGCGG 215
QY      140 YAspTyArgValSerHisGluLeuMetHisHisGlnArgArgArgAlaValAlaValSer 160
DB      216 CGATTACGTGTCCCATGAATATCATGCACCATCAGCGGCGGAGAAAGACAGTGGCGTGC 275
QY      160 rGluValGluSerLeuHisLeuArgLeuLysGlyProArgHisAspPheHisMetAspLeu 180
DB      276 CGAGGTGAGTCTCTTCACTTCGCGCTGMAAGGCTCCAGGCAAGCTTCCACGTGATCT 335
QY      180 uArgThrSerSerSerLeuValAlaProGlyPheIleValGlnThrLeuGlyLysThrGln 200
DB      336 GAGGACTTCCAGCAGCCTAGTGGCTCCTGGCTTATTGTGCAGACGTTGGAAAGACAGG 395
QY      200 YThrLysSerValGlnThrLeuProProGluAspPheCysPheTyrglnGlySerLeuArg 220
DB      396 CACTAAGTCTGTGCAGACTTTACCGCCAGAGGACTTCTGTTCTATCAAGGCTCTTTGCG 455
QY      220 gSerHisArgAsnSerProSerHisGlyGlyLysPheCysGluGlySerThrArgThrIle 240
DB      456 ATCACACAGAACTCC--TCAGTGGCCCTTTCAACCTGCCAAGGCTGTGCAGGCATGAT 512
QY      240 uLysLeuCysAsnSerGlnLysCysProArgAspSerValAspPheArgAlaAlaGlnCys 260
DB      513 ACGA-----ACAGAAAGGCAAGATTACTTCTTAAGGCCACT 548
QY      260 sAlaGluHisAsnSerArgArgPheArgGlyArgHisTyrrLysTrpLysProTyrrThrGln 280
DB      549 TCCTTCACACCTCTCA-----TGAAA----- 570
QY      280 nValGluAlaAspLeuCysLysLeuTyrrCysIle-AlaGluGlyPheAspPhePhePhe 300
DB      571 -----CTCGGCAAG----- 580
QY      300 erLeuSerAsnLysValLysAspGlyThrProCysSerGluAspSerArgAsnValCysI 320
DB      581 --CTGCCCAAGGCAAGCTCGCCATCCCACTACTGTACAAGAGATCCACAGAGCCCATGC 638
QY      320 leAspGlyIleCysGluLeuSerValValSerThrSer-----AlaHis----- 334
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DB      639 TCCT-GGGGCCAGTGAAGCTCTGTGTGACTCAAGACATGGGAGCTGGACATCAACCCC 697
QY      334 ----- 334
DB      698 TGCAACAGCAGCAGCTTCGCTCGGACTGCCACAAAGACAGCATTTCTGTGAAGACGCA 757
QY      335 -----MetProGlnProProLysGluAspLeuPheIleLeuProAspGluTyrrLys 352
DB      758 AGAATATACATGCCCGCAGCCTCCCAAGAGAAGACTTTCATCTTGCCAGATGAGTATAAGT 817
QY      352 erCysLeuArgHisLysArgSerLeuLeuArgSerHisArgAsnGluLeuAsnValG 372
DB      818 CTGTCTTACGGCATTAAGCCTCTCTTGTAGAGTCCCATAGAATGAAGAATGAACGTGG 877
QY      372 luThrLeuValValValAspLysLysMetMetGlnAsnHisGlyHisGluAsnIleThrT 392
DB      878 AGACCTTGTTGGTGGTGCACAAAGATGATGCAAAGCATGGCCATGAATAATATCACCA 937
QY      392 hrTyrrValLeuThrIleLeuAsnMetValSerAlaLeuPheLysAsp----- 407
DB      938 CCTACGTGCTCAGCATACTCAACATGGTATCTGCTTATTCAAGATGGAACAATAGAG 997
QY      407 ----- 407
DB      998 GAAACATCAACATTGCAATTGTAGGTGTGATTCTTCTAGAAGATGAACAGCAGACTGG 1057
QY      408 -----GlyLeuM 410
DB      1058 TGATAAGTCACCAAGCAGACCAACACCTTAAGTAGCTTCTGCCAGTGGCAGTCTGGATTGA 1117
QY      410 etGlyLysAspGlyThrArgHisAspHisAlaIleLeuLeuThrGlyLeuAspIleCys 430
DB      1118 TGGGGAAGATGGGACTGTCATGACCAAGCCATCTTAAGTGTGATATATGTT 1177
QY      430 erTrpLysAsnGluProCysAspThrLeuGlyPheAlaProIleSerGlyMetCysSerL 450
DB      1178 CCTGGAAGATGAGCCCTGTGACACTTTGGGATTTGCCACCCATTAAGTGAATGTGTAGTA 1237
QY      450 ysTyrrArgSerCysThrIleAsnGluAspThrGlyLeuGlyLeuAlaPheThrIleAlaH 470
DB      1238 AATATCCGACGTGCACGATTAATGAAGATACAGGTTCTTGGACTGGCCTTCAACATTGCC 1297
QY      470 isGluSerGlyHisAsnPheGlyMetIleHisAspGlyGluGlyAsnMetCysLysLys 490
DB      1298 ATGAGTCTGCACACAACCTTTGGCATGATTCATGATGGAGAAAGGAAACATGTGTAAAGT 1357
QY      490 erGluGlyAsnIleMetSerProThrLeuAlaGlyArgAsnGlyValPheSerTrpSerP 510
DB      1358 CCGAGGGCAACATCATGTCCCTACATTGGCAGAGCAATGGAAGTCTTCTCCTGTCTAC 1417
QY      510 roCysSerArgGlnTyrrLeuHisLysPheLeuSerThrAlaGlnAlaIleCysLeuAla 530
DB      1418 CCTGCAGCCGCCAGTATCTACACAATTTCTAAGCACCGCTCAAGCTTATCTGCTGTCTG 1477
QY      530 sPGLnProLysProValLysGluTyrrLysTyrrProGluLysLeuProGluLeuTyrrA 550
DB      1478 ATCAGCCAAAGCCTGTGAAGGAATACAGTATCCTGAGAAATTGCCAGAGAATTAATATG 1537
QY      550 sPalaAsnThrGlnCysLysTrpGlnPheGlyGluLysAlaLysLeuCysMetLeuAspP 570
DB      1538 ATGCAACACACAGTGAAGTGGCAGTTCCGAGAGAAAGCCAAAGCTTGCATGCTGGACT 1597
QY      570 heLysLysAspIleCysLysAlaLeuTrpCysHisArgIleGlyArgLysCysGluThrL 590
DB      1598 TTAAAGAGACATCTGTAAAGCCCTGTGGTGCATCGTATTGGAAGAAATGTAGACTTA 1657
QY      590 ysPheMetProAlaAlaGluGlyThrIleCysGlyHisAspMetTrpCysArgGlyGlyG 610
DB      1658 AATTTAATGCCAGCAGCAGAAAGCACAAATTTGTGGGCATGACATGTGGCGGAGAGAC 1717
QY      610 lncysValLysTyrrGlyAspGluGlyProLysProThrHisGlyHisTrpSerAspTrpS 630
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Db 1718 AGTGTGTGAATATGATGTAAGGCCCAAGCCCAACCATGCGCACTGTCGACTGGT 1777
QY 630 eSerTrpSerProCysSerArgThrCysGlyGlyValSerHisArgSerArgLeuC 650
Db 1778 CTTCTTGTCCTCCCATGCTCCAGAGACTGCGGAGGGGAGTATCTCATAGAGTCCGCTCT 1837
QY 650 YeThrAsnProLysProSerHisGlyGlyLysPheCysGlyGlySerThrArgThrLeuL 670
Db 1838 GCACCAACCCCAAGGCATCGCATGGAGGGAAGTTCTGTGAGGGCTCCACTCGACTCTGA 1897
QY 670 YeLeuCysAsnSerGlnLysCysProArgAspSerValAspPheArgAlaIaGlnCysA 690
Db 1898 AGCTCTGCACAACAGTGAAGAATGTCCCGGGGACAGTGTGACTTCGCTGCTGCTGCTG 1957
QY 690 IaGluHisAsnSerArgArgPheArgGlyArgHisGlyTrpLysTrpLysProTyrThrGlnV 710
Db 1958 CCGAGCAACAACAGCAGATTCAGAGGGGCGGCACTACAAGTGAAGCCTTACACTCAAG 2017
QY 710 aIaGluAspGlnAspLeuCysLysLeuTyrCysIleAlaGluGlyPheAspPhePheS 730
Db 2018 TAGAAGATCAGAGCTTATGCAAACTCTACTGTATCGCAGAAGATTGATTCTCTTTT 2077
QY 730 eLeuSerAsnLysValLysAspGlyThrProCysSerGluAspSerArgAsnValCysI 750
Db 2078 CTTTGTCAATTAAGTCAAAAGATGGGACTCCATGCTCGGAGGATACCCGTAATGTTGTA 2137
QY 750 IaAspGlyIleCysGlyArgValGlyCysAspAsnValLeuGlySerAspAlaValGluA 770
Db 2138 TAGATGGGATATGTGAGAGAGATTGGATGTGACAAATGTCCTTGATCTGATGCTTTGAAG 2197
QY 770 spValCysGlyValCysAsnGlyAsnAsnSerAlaCysThrIleHisArgGlyLeuTyrT 790
Db 2198 ACCTCTGGGGGTGTGTAAACGGGAATACTACGCTGCACAGATTCAAGGGGTCTCTACA 2257
QY 790 hTrLysHisHisThrAsnGlnTyrTrpHisMetValThrIleProSerGlyAlaArgS 810
Db 2258 CCAAGCACCAACCAACCAAGTATTATCACATGATCACCATTCCTTCTGAGCCCGGA 2317
QY 810 eTrIleArgIleTyrGluMetAsnValSerThrSerTyrIleSerValArgAsnAlaLeuA 830
Db 2318 GTATCCGCATCTATGAATGAACGCTCTTACCTCTACATTCTGTGCGCAATGCCCTCA 2377
QY 830 rGArgTyrTyrLeuAsnGlyHisTrpThrValAspTrpProGlyArgTyrLysPheSerG 850
Db 2378 GAAGGTACTACCTGAATGGGCACCTGGACCGTGGACTGGCCCGCGGTACAATAATTTTCGG 2437
QY 850 lYThrThrPheAspTyrArgArgSerTyrAsnGluProGluAsnLeuIleAlaThrGlyP 870
Db 2438 GCACTACTTTCGACTACAGACGGTCTTATATGAGCCCGAGAATTAAATCGCTACTGGAC 2497
QY 870 roThrAsnGluThrLeuIleValGluLeuLeuPheGlnGlyArgAsnProGlyValAlaT 890
Db 2498 CAACCAACGAGACACTGATTGTGAGCTGTGTTTCAGGGAAGAACCCGGGTGTGCTT 2557
QY 890 rPgluTyrSerMetProArgLeuGlyThrGluLysGlnProProAlaGlnProSerTyrT 910
Db 2558 GGGATACTCCATGCTCGCTTGGGACCGAAGACAGCCCTGCCCCAGCCCACTACA 2617
QY 910 hTrTrpAlaIleValArgSerGluCysSerValSerCysGlyGlyArg 926
Db 2618 CTTGGGCCATCGTGGCTCTGAGTGTCTCGTCTCGCGAGGGGAGACAG 2667

RESULT 9
US-10-217-774-5
; Sequence 5, Application US/10217774
; Publication No. US20020193583A1
; GENERAL INFORMATION:
; APPLICANT: Fiddler, Carl Johan
; APPLICANT: Hilbun, Erin
; TITLE OF INVENTION: No. US20020193583A1e1 Human Proteases and Polynucleotides Encodir
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0219-USA
; CURRENT APPLICATION NUMBER: US/10/217,774

; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US/09/930,872
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/225,852
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4042
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-217-774-5

Alignment Scores:
Pred. No.: 0 Length: 4042
Score: 3981.50 Matches: 764
Percent Similarity: 78.26% Conservative: 17
Best Local Similarity: 76.55% Mismatches: 38
Query Match: 76.04% Indels: 181
DB: 13 Gaps: 10

US-09-981-151D-8 (1-952) x US-10-217-774-5 (1-4042)

QY 1 MetLysProArgAlaArgGlyTrpArgGlyLeuAlaAlaLeuTrpMetLeuAlaGln 20
Db 99 ATGAAGCCCCCGCGCGCGGATGGCGGGCTTGGCGCGCTGTGTGATGCTGTGGCGCAG 158
QY 21 ValAlaGluGlnValSerProGlyArgSerHisGlnArgGlyAsnArgGlySerGlyGln 40
Db 159 GTGGCCGAGCA----- 169
QY 41 LeuGluAlaSerProProArgLeuLeuSerArgGlyProArgArgLeuThrAlaMetSer 60
Db 169 ----- 169
QY 61 ProLeuPheSerAlaGlyThrCysValArgHisGlyThrArgSerGlySerAlaTrpGlu 80
Db 170 -----GGCACTGCGGTGCGCATGGGAGACCCGCGAGCGGACGCCCTGGGAG 214
QY 81 ProGluArgProAlaSerSerSerThrArgGlyAlaAlaGlyLeuAspGly-LysGlyAr 100
Db 215 CCCGAGCGTCCCGCGTCTCTCTCCACCCGCGGAGCGCGCGGCTGGATGMAAAGGC-- 272
QY 100 GasPmetAspGluAlaGlyAsnHisArgSerGlnGlnThrAsnThrGlyThrGluAsnG 120
Db 272 ----- 272
QY 120 nThrLeuHisValLeuThrGlnTyrAspLeuValSerAlaTyrGluValAspHisArgG 140
Db 273 -----GATATAGACCTGTCTCTGCTACGAGGTTGACACACAGGGG 313
QY 140 YAspTyrValSerHisGluIleMetHisHisGlnArgArgArgAlaValAlaValSe 160
Db 314 CGATTACGTGTCCCATGAATCATGACCATCAGCGCGGAGAAAGACAGTGGCCGTGTC 373
QY 160 rGluValGluSerLeuHisLeuArgLeuLysGlyProArgHisAspPheHisMetAspLe 180
Db 374 CGAGGTGAGTCTCTTCACTTCGCGCTGAAGGCTCCAGGCAAGACTTCCACGTGATCT 433
QY 180 uArgThrSerSerSerLeuValAlaProGlyPheIleValGlnThrLeuGlyLysThrG 200
Db 434 GAGGACTTCCAGCAGCCTAGTGGCTCTGCGCTTTATTGTGACAGACGTTGGAAAGACAGG 493
QY 200 YThrLysSerValGlnThrLeuProProGluAspPheCysPheTyrGlnGlySerLeuAr 220
Db 494 CACTAAGTCTGTGCAAGACTTAAACGCCAAGAGACTTCTGTTCATCAAGGCTCTTGGC 553
QY 220 gSerHisArgAsnSerProSerHisGlyGlyLysPheCysGlyGlySerThrArgThrLe 240
Db 554 ATCACACAGAAACTCC--TCAGTGGCCCTTTCACCTGCCCAAGGCTTGTGAGGCATGAT 610
QY 240 uLysLeuCysAsnSerGlnLysCysProArgAspSerValAspPheArgAlaIaGlnCy 260
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Db 611 AGCA-----ACAGAGAGCGAGATTACTTCTTAAGGCCACT 646
Qy 260 sAlaGlUHiSaNsErArGaRhpEaRgGlYaRgHiStYrLySTrPlySProTYrThRgI 280
Db 647 TCCTTCACACCTCTCA-----TGAAA----- 668
Qy 280 nValGlUAlaSpLeuCysLySLeuTYrCySiLe-AlaGlUgLyPheAspPhePheS 300
Db 669 -----CTCGCAGAG----- 678
Qy 300 eRLeuSeRAsnLySValLySaSpGlyThRProCySSeRgLuAspSeRArgAsnValCySi 320
Db 679 --CTGCCCAAGGAGCTCGCCATCCACGTACTGTACAAAGAGATCCACAGAGCCCATGC 736
Qy 320 lEaSpGlylLeCySgLuLeuSeRValSeRThRSeR-----AlaHiS----- 334
Db 737 TCCT- GGGGCCAGTAGGTCCTGGTGACCTCAAGACATGGGAGCTGCACATCAACCCC 795
Qy 334 ----- 334
Db 796 TGCACAGACGACCTTCGCTGGAGCTGCCAACAAGACAGCATTTCTGTGAAGACGCA 855
Qy 335 -----MetProGlnProProLySGluAspLeuPheIlLeuProAspGluTYrLyS 352
Db 856 AGAATACATGCCCCAGCCTCCCAAGAGACCTTTCATCTTGCCAGATGATATAAGT 915
Qy 352 eRCysLeuARgHiSlYsARgSeRleuLeuARgSeRHiSARgAsnGlUgLuLeuAsnValG 372
Db 916 CTGCTTACGGCATAAAGCGCTCTCTTCTGAGGTCCTCATAGAAATGAAGAACTGAACGTGG 975
Qy 372 lUthrLeuValValAlaSpLySlySMeCMeGlAsnHiSgLyHiSgLuAsnIlLeThRt 392
Db 976 AGACCTTGtGtGtGtGCACAAAGATGATGCAAAACCATGCGCATGAATAATCACCA 1035
Qy 392 hRtYrValLeuThrIlLeuAsnMeCValSeRAlaLeuPheLySAsp----- 407
Db 1036 CTTACGTGCTCAGATACTCAACATGTATCTGCTTATTCAAAGATGAACAATAGAG 1095
Qy 407 ----- 407
Db 1096 GAAACATCAACATTGCAATTGTAGTCTGATTCTTAGAAGATGAACAGCCAGACTGG 1155
Qy 408 -----GlyLeuM 410
Db 1156 TGATAAGTCAACGACGACGACCAACCTTAAGTAGCTTCTGCCAGTGCAGCTGTGATTGA 1215
Qy 410 eCgLyLySaSpGlyThRARgHiSaSPHiSaAlaIlLeuLeuThRgLyLeuAspIlLeCyS 430
Db 1216 TGGGGAAGAATGGGACTCGTGTATGACCAAGCCATCTTACTGACTGTGTGATATATGTT 1275
Qy 430 eRTPrLySaSnGlUProCySaSpThRleuGlYPheAlaProIlSeRgLyMeTCysSeRt 450
Db 1276 CTTGGAAGAATGAGCCCTGTGACACTTTGGATTGGACCCCAATAGTGAATGTAGTA 1335
Qy 450 ySTYrARgSeRCysThRlLeaSnGlUAspThRgLyLeuGlYLeuAlaPheThRlLeAlaH 470
Db 1336 AATATCGACGCTGCACGATTAATGAAGATACAGGTCCTTGACTGGCCTTCAACATTGCC 1395
Qy 470 lSgLUsErGlyHiSaSnPheGlyMeCilLeHiSaSpGlyGlUgLyAsnMeTCySlySlyS 490
Db 1396 ATGAGTCTGCACACAACCTTGGCATGATTCAATGATGAGAGGAACAATGTAAAAAGT 1455
Qy 490 eRgGlUgLyAsnIlLeMeSeRProThRleuAlaGlYARgAsnGlYAlPheSeRTPrSeR 510
Db 1456 CCGAGGGCAACATCATGTCCCTACATGGGAGACGCAATGAGTCTTCCTGTGTAC 1515
Qy 510 rOCysSeRArgGlnTYrLeuHiSlYsPheLeuSeRThRAlaGlAlaIlLeCySleuAla 530
Db 1516 CCTGCAGCCGCGAGTATCTACAAATTTCTAAGCACCGCTCAAGCTATGCTCTGCTG 1575
Qy 530 sPGLnProLySProVallySeGlUTYrLySTYrProGluLyLeuProGlyGluLeuTYrA 550
Db 1576 ATCAGCCAAAGCCTGTGAAGGAAATACAGTATCCTGAGAAATTGCCAGAGAAATTATATG 1635

Qy 550 sPAlaEnThRglnCySlySTPrGlnPheGlyGlUlyValAlaLySLeuCysMeTLeuAsp 570
Db 1636 ATGCAACACACAGCTGCAGTGGCAGTTCGGAGAGAAACCAAGCTCTGCATGCTGACT 1695
Qy 570 hElYsLySaSpIlLeCySlySaAlaLeuTPrCySHiSaRgIlLeGlYARgLyS CySgLuThRt 590
Db 1696 TTA AAAAGACATCTGTAAAGCCCTGTGTGCCATCGTATTGGAGGAATGTGAGACTA 1755
Qy 590 ySPheMeRProAlaAlaGlUgLyThRlLeCySgLyHiSaSpMeTTrPCySaRgGlYg 610
Db 1756 AATTATGCCACGACGAGAAAGCAACAATTTGTGGGCATGACATGTGTGTCCGGGAGGAC 1815
Qy 610 lncYsVallySTYrGlyAspGlUgLyProLySProThRHiSgLyHiSTPrSeRAspTrPS 630
Db 1816 AGTGTGTAAATATGTGTGATGAAGGCCCCAAGCCCATGCGCACTGTGTGGACTGGT 1875
Qy 630 eRSeRTPrSeRProCySSeRArgThRCySgLyGlYValSeRHiSaRgSeRArgLeuC 650
Db 1876 CTTCTTGCTCCCATGCTCCAGGACCTGCGGAGGGGAGTATCTCATAGGAGTCCCTCT 1935
Qy 650 ySThRAsnProLySProSeRHiSgLyGlyLySPheCySgLuGlySeRThRArgThRLeuL 670
Db 1936 GCACCAACCCCAAGCCATCGCATGAGGGAAGTTCTGTGAGGGCTCCACTCGCACTGTGA 1995
Qy 670 ySLeuCysAsnSeRglnLySCysProARgAspSeRValaSpPheARgAlaAlaGlncYsa 690
Db 1996 AGCTCTGCACACAGTCAAGAAATGTCCCCGGGACAGTGTGACTTCCGTGCTCACTGTG 2055
Qy 690 lAgLUHiSaNsErARgARhpEaRgGlYARgHiSTYrLySTPrLySProTYrThRglnV 710
Db 2056 CCGAGCACACAGACAGCAGATTCAAGAGGGCGGCACTACAGTGAAGCCTTAACACTCAAG 2115
Qy 710 aGlUAspGlnAspLeuCysLySLeuTYrCySiLeaGlUgLyPheAspPhePhePheS 730
Db 2116 TAGAAGATCAGGACTTATGCAAACTTACTGATCCGAGAAAGATTGATTCTTCTTTT 2175
Qy 730 eRLeuSeRAsnLySVallySaSpGlyThRProCySSeRgLuAspSeRArgAsnValCySi 750
Db 2176 CTTGTCAATAATAAGTCAAAAGATGGGACTCCATGCTCGAGAGATAGCCGTATGTGTGA 2235
Qy 750 lEaSpGlylLeCySgLuARgValGlyCySaSPAsnValLeuGlYSeRAspAlaValGlUa 770
Db 2236 TAGATGGATATATGTAGAGAGTTGGATGTGACAAATGCTTGGATCTGATGCTGTGAAG 2295
Qy 770 sPValCySgLyValCySaSnGlYAsnAsnSeRAlaCySThRlLeHiSaRgGlYLeuTYrT 790
Db 2296 ACGTCTGTGGGGTGTGTAACGGAATAACTCAGCCTGCACGATTCAAGGGGTCTCTACA 2355
Qy 790 hRtLySHiSHiSThRAsnGlNTYrTYrHiSMeCValThRlLeProSeRgLyAlaArgS 810
Db 2356 CCAAGCACCAACACCAACAGATATTATCACATGTGCACCATTCCTTCTGGAGCCCGGA 2415
Qy 810 eRlLeARgIlLeTYrGlUMeCAsnValSeRThRSeRTYrIlSeRValARgAsnAlaLeuA 830
Db 2416 GTATCCGATCTATGAATGAACGCTCTACCTCTACATTCTGTGTGCCAATGCCCTCA 2475
Qy 830 rGARgTYrTYrLeuAsnGlYHiSTPrThRValaSpTrPProGlyARgTYrLySPheSeRg 850
Db 2476 GAAGTACTACCTGAATGGGCACTGCACCGTGAAGTGGCCCGGCGGTAAATTTTCGG 2535
Qy 850 lYThRThRPhEaSPTYrARgARgSeRTYrAsnGlUProGluAsnLeuIlAlaThRgLyP 870
Db 2536 GCACTACTTTGCACACTACAGACGGTCTCTAATAGAGCCGAGAACTTAATCGCTACTGAC 2595
Qy 870 rOThRAsnGlUThRleuIlValGlUleuLeuPheGlnGlYARgAsnProGlyValAlaT 890
Db 2596 CAACCAACGAGACACTGATTGTGAGCTGTGTTCAGGGAAGAACCCGGGTGTGCT 2655
Qy 890 rPGLnTYrSeRMeCProARgLeuGlYThRgLuLySglnProProAlaGlnProSeRTYrT 910
Db 2656 GGAATACTCCATGCTCGCTTGGGACCGAGAAAGACCCCTGCCAGCCAGCTACA 2715

Db 1336 AATATCGCAGCTGCACGATTAAATGAGATACAGGCTTGGACTGGCCTTCACCAATTGCCC 1395
QY 470 IAGLUSerGIYHISAsnPheGIYMetIleHISAspGIYGLUGIYAsnMetCysLYsLYS 490
Db 1396 ATGAGTCTGGACACAACCTTTGGCATGATTCATGATGAGAGAGGAACATGTGTAATAAGT 1455
QY 490 eRGLUGIYAsnIleMetSerProThrLeuAlaGIYArgAsnGIYValPheSerTrpSerP 510
Db 1456 CCGAGGGCAACATCATGTCTCCCTTACATTGGCAGAGACGCAATGAGATCTTCTCTGCTCAC 1515
QY 510 rOCysSerArgGIYTrpLeuHISLYSPheLeuSerThrAlaGlnAlaIleCysLeuAlaA 530
Db 1516 CTTGCAGCCGGCAGATATTCTACAAATTTCTAAGCACCGCTCAAGCTATCTGCTTGCTG 1575
QY 530 sPGLnProlYsProValLYSGIYTrpLYSTYrProGluLYSLeuProGluLYLeuTYrA 550
Db 1576 ATCAGCCAAAGCCTGTGAGAGGATACAAAGTATCTGAGAAATTCAGAGGAATTATATG 1635
QY 550 sPAlaAsnThrGlnCYsLYSTrPGLnPheGIYGLULysAlaLYSLeuCYsMetLeuAspP 570
Db 1636 ATGCAAAACACAGTGCAGAGTGCAAGTGCGAGTTCGGAGAGAAAGCCAAAGCTTCAGTGCAGACT 1695
QY 570 heLYsLYsAspIleCYsLYsAlaLeuTrpCYsHISArgIleGIYArgLYsCYSGluThrL 590
Db 1696 TTAAAAAGGACATCTGTAAAGCCCTGTGTGTCATCGTATTGGAAAGAAATGTGAGACTA 1755
QY 590 YsPHeMetProAlaAlaGLUGIYThrIleCYSGIYHISAspMetTrpCYsArgGIYGLYg 610
Db 1756 AATTATGCCAGACAGCAGAGGACCAATTGTGGGCAATGACATGTGTGCCGGGAGAGAC 1815
QY 610 lNCysValLYSTYrGIYAspGIUGIYProLYsProThrHISGLYHISTrpSerAspTrps 630
Db 1816 AGTGTGTAATATGTGTGATGAAGGCCCCCAAGCCCAACCATGCGCACGTGCGGACTGGT 1875
QY 630 eRSeTrpSerProCYsSerArgTrpCYSGIYGLIYValSerHISArgSerArgLeuc 650
Db 1876 CTTCTTGTCCTCCATGCTCCAGAACCTGCGGAGGGGAGATTCATAGAGATCGCCTCT 1935
QY 650 YsThrAsnProLYsProSerHISGLIYLYsPheCYSGIUGIYSerThrArgTrpLeuL 670
Db 1936 GCACCAACCCCAAGCCATCGCATGAGAGGAGTTCTGTGAGGGCTCCACTGCACACTCTGA 1995
QY 670 YsLeuCYsAsnSerGlnLYsCYsProArgAspSerValAspPheArgAlaIaGlnCYsA 690
Db 1996 AGCTCTGCAACAGTCAGAAATGTCCCGGGACAGTGTGACTTCGCTGCTCAGTGTG 2055
QY 690 lAGlUHISAsnSerArgArgPheArgGLYArgHISTrpLYSTYrTrpLYsProTYrThrGlnV 710
Db 2056 CCGAGCACAAACAGCAGACGATTCAGAGGGCGGCACTACAAGTGGAAGCCCTTAACACTCAAG 2115
QY 710 aIGlUAspGlnAspLeuCYsLYsLeuTYrCYsIleAlaGLUGIYPheAspPhePheS 730
Db 2116 TAGAAGATCAGGACTTATGCAAACTCTACTGTATCGCAGAGGATTTGATTTCTTCTTTT 2175
QY 730 eRLeuSerAsnLYsValLYsAspGIYThrProCYsSerGluAspSerArgAsnValCYsI 750
Db 2176 CTTTGTCAATTAAGTCAAGAGATGGAGACTCATGCTCGGAGGATAGCCGTAATGTTGTA 2235
QY 750 lEAspGIYIleCYSGIUAArgValGIYCYsAspAsnValLeuGIYSerAspAlaValGIUA 770
Db 2236 TAGATGGGATATGTGAGAGAGTTGGATGTGCAATGTCTTGATCTGATCTGTTGAAG 2295
QY 770 sPValCYSGIYValCYsAsnGIYAsnAsnSerAlaCYSThrIleHISArgGIYLeuTYrT 790
Db 2296 ACGTCTGTGGGGTGTGAACGGGAATAACTCAGCCTGCAGCATTCACAGGGGTCTCTACA 2355
QY 790 hRLYSHISHisThrAsnGlnTYrTYrHISMetValThrIleProSerGIYAlaArgS 810
Db 2356 CCAAGCACCAACACCAACAGATATATCATGTGCACCATTCCTTCGAGAGCCCGGA 2415
QY 810 eRlLeArgIleTYrGluMetAsnValSerThrSerTYrIleSerValArgAsnAlaLeuA 830
Db 2416 GTATCCGCACTCTATGAATGAAGCTCTCTACTCTCTACATTTCTGTGCGCAATGCCCTCA 2475

QY 830 rGArgTYrTYrLeuAsnGIYHISTrpThrValAspTrpProGluYArgTYrLYsPheSerG 850
Db 2476 GAAGGTACTAACCCTGAATGGGCACTGGACCGCTGGACTGGCCCCGGGTACAAATTTCCG 2535
QY 850 lYThrThPheAspTYrArgArgSerTYrAsnGluProGluAsnLeuIleAlaThrGLYp 870
Db 2536 GCACTACTTTCGACTACAGACGGTCTCTAATAGAGCCCGAGAACTTAATGCTACTGGAC 2595
QY 870 rOThrAsnGluThrLeuIleValGIUleuLeuPheGlnGIYArgAsnProGluYValAlaT 890
Db 2596 CAACCAAGAGACACTGATTTGTGAGCTGCTGTTCAAGGAGAAAGAACCCGGGTGTTGCC 2655
QY 890 rPGLUYrSerMetProArgLeuGIYThrGluLYSGlnProProAlaGlnProSerTYrT 910
Db 2656 GGAATACTCCATGCTGCTGCTTGGGGACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2715
QY 910 hRTPrAlaIleValArgSerGluCYsSerValSerCYSGIYGLIYArg 926
Db 2716 CTTGGCCATCGTGCCTCTGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2765

RESULT 11
US-09-981-151A-5
; Sequence 5, Application US/09981151A
; Publication No. US20030212256A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Gerlach, Valerie
; APPLICANT: MacDougall, John R
; APPLICANT: Malyanakar, Muriel M
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John A
; APPLICANT: Stone, David J
; APPLICANT: Gunther, Erik
; APPLICANT: Ellerman, Karen
; APPLICANT: Shimkets, Richard A
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Guo, Xiaojia
; APPLICANT: Patturajan, Meera
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Burgess, Catherine E
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Gangolli, Esha A
; APPLICANT: Fernandes, Elma R
; APPLICANT: Gorman, Linda
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-168
; CURRENT APPLICATION NUMBER: US/09/981,151A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 60/241,040
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,058
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,063
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/241,243
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/242,152
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/242,482
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,611
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,612
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/242,880
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/242,881
; PRIOR FILING DATE: 2000-10-24
; Remaining Prior Application data removed - See File Wrapper or PALM.

QY 557 pGlnPheGlyGluLysAlaLysLeuCysMetLeuAspPheLysLysAspIleCysLysAla 577
DB 1597 GCAGTTCCGAGAGAAAGCCCAAGCTCTGCATGCTGGAACTTTAAAAAGACATCTGTAAGC 1656
QY 577 aLeuTrpCysHisArgIleGlyArgLysCysGluThrLysPheMetProAlaAlaGluG 597
DB 1657 CCTGTGTGCCATCTGATTGTGAAGAAATGTGAGACTAAATTATATGCGACAGCAGAGG 1716
QY 597 YThrIleCysGlyHisAspMetTrpCysArgGlyGlyGlnCysValLysTrpGlyAspG 617
DB 1717 CACAATTGTGGGCATGACAA-TGGTGCC--GGAGGACAGTGTGTGAATATGTTGATGA 1773
QY 617 uGlyProLysProThrHisGlyHisTrpSerAspTrpSerSerTrpSerProCysSerAr 637
DB 1774 AGGCCCCAAGCCCAAGCCCATGGCCACTGGTCGACTGGTCTTGTGTCCTCCCATGCTCCAG 1833
QY 637 gThrCysGlyGlyGlyValSerHisArgSerArg---LeuCysThrAsnProLysProse 656
DB 1834 GACCTGCGAGGGGAGTATCTCATAGAGTCGCTCTCAAAATACACATTCCAGGCCATC 1893
QY 656 rHisGlyGlyLysPheCysGlyGlySerThrArgThrLeuLysLeuCysAsnSerGlnLy 676
DB 1894 GCATGAGGGAAGTTCTGTGAGGGCTCCACTGCGACTCTGAAGCTCTGCAACAGTCAGAA 1953
QY 676 sCysProArgAspSerValAspPheArgAlaAlaGlnCysAlaGluHisAsnSerArgAr 696
DB 1954 ATGTCCCCGGGACAGTGTGACTCTCCGTGCTGCTCAGTGTGCCGAGCACAAACAGCAGACG 2013
QY 696 gPheArgGlyArgHisTrpLysTrpLysProTrpThrGlnValGluAspGlnAspLeuCy 716
DB 2014 ATTCAGAGGGCGGCACATACAGTGAAGCCT-----GATCAGCACTTATG 2058
QY 716 sLysLeuTrpCysIleAlaGluGlyPheAspPhePheSerLeuSerAsnLysValLy 736
DB 2059 CAACTCTACTGTATCGCAGAGGATTTGATTCTTCTTTCTTGTCAATAAAGTCAA 2118
QY 736 sAspGlyThrProCysSerGluAspSerArgAsnValCysIleAspGlyIleCysGlyAr 756
DB 2119 AGATGGGACTCCATGCTCGGAGGATAGCCGTAATGTTGTATAGATGGATATGTGAGAG 2178
QY 756 gValGlyCysAspAsnValLeuGlySerAspAlaValGluAspValCysGlyValCysAs 776
DB 2179 AGTTGATGTGACAAATGCTCTTGATCTGATGCTGTTGAAGACGTCGTGTGGGTGTGAA 2238
QY 776 nGlyAsnAsnSerAlaCysThrIleHisArgGlyLeuTrpThrLysHisHisIsthrAs 796
DB 2239 CGGGAATACTCAGCCTGCAGATTCACAGGGGTCTCTACCTA----- 2281
QY 796 nGlnTrpThrHisMetValThrIleProSerGlyAlaArgSerIleArgIleTrpGluMe 816
DB 2282 -GAGTATTATCACATGTGTCAACATTCTTGTGGAAGCCCGAGTATCCGCATCTATGAAT 2340
QY 816 tAsnValSerThrSerTrpIleSerValArgAsnAlaLeuArgArgTrpTrpLeuAsnG 836
DB 2341 GAACGTCTTAACCTCTACATTCTGTGCGCAATGCCCTCAGAAAGTACTACTGAATGG 2400
QY 836 yHisTrpThrValAspTrpProGlyArgTrpLysPheSerGlyThrThrPheAspTrpAr 856
DB 2401 GCACTGAGCCGTGACTGGCCCGCGGTACAAATTTTCGGGCACTACTTTCGACTACAG 2460
QY 856 gArgSerTrpAsnGluProGluAsnLeuIleAlaThrGlyProThrAsnGluThrLeuI 876
DB 2461 ACGGTCTTAATAGAGCCCGAAGAACTTAATGCTACTGACCAACCAAGACGACTGAT 2520
QY 876 eValGluLeuLeuPheGlnGlyArgAsnProGlyValAlaTrpGluTrpSerMetProAr 896
DB 2521 TGTGAGAGTGTGTTTCAGGGAAGAAACCGGGTGTGCTCGGGAATATCTCATGCCCTCG 2580
QY 896 gLeuGlyThrGluLysGlnProProAlaGlnProSerTrpThrTrpAlaIleValArgSe 916
DB 2581 CTTGGGAGACGAGAGCAGCCCTGCGCCAGCCAGCTACACTTGGGCCATCGTGGCGTC 2640
QY 916 rGluCysSerValSerCysGlyGlyGlyArgCysLeuProValLeuLeuGluAlaAl 936

DB 2641 TGAGTGTCTCGTGTCTCTGGAGAGGGGTAGGTGCTTCCAGTGTGCTCTCTGGAGGACG 2700
QY 936 aCysGlnProSerAlaThrAlaTrpIleAlaLeuAlaPheLeuGluSer 952
DB 2701 ATGTCAAGCTTTAGCCACTGCGTACATTCGACTGCGCTTCTTGAATCC 2749

RESULT 12

US-10-399-645-19
; Sequence 19, Application US/10399645
; Publication No. US20040029249A1
; GENERAL INFORMATION:

; APPLICANT: INCYTE CORPORATION; LEE, Ernestine A.
; APPLICANT: HAFALIA, April J.A.; YUE, Henry
; APPLICANT: LAL, Preeti G.; YAO, Monique G.
; APPLICANT: LU, Yan; CHAWLA, Narinder K.
; APPLICANT: WARREN, Bridget A.; LU, Dyung Aina M.
; APPLICANT: BAUGHN, Mariah R.; DELEGANE, Angelo M.
; APPLICANT: BURFORD, Neil; BOROWSKY, Mark L.
; APPLICANT: LEE, Sally; XU, Yuming
; APPLICANT: GRIFFIN, Jennifer A.; KALLICK, Deborah A.
; APPLICANT: GANDHI, Ameena R.; ARVIZU, Chandra S.
; APPLICANT: ISON, Craig H.; TANG, Y. Tom
; APPLICANT: AZIMZAI, Yalda; ELLIOTT, Vicki S.
; APPLICANT: SWARNAKAR, Anita; RAMKUMAR, Jayalaxmi
; APPLICANT: NGUYEN, Daniel B.; TRIBOULEY, Catherine M.
; APPLICANT: LO, Terence P.; AU-YOUNG, Janice K.
; APPLICANT: THANGAVELU, Kavitha; KEARNEY, Liam

; TITLE OF INVENTION: PROTEASES

; FILE REFERENCE: PI-0263 USN

; CURRENT APPLICATION NUMBER: US/10/399, 645

; CURRENT FILING DATE: 2003-04-16

; PRIOR APPLICATION NUMBER: PCT/US01/51034

; PRIOR FILING DATE: 2001-10-18

; PRIOR APPLICATION NUMBER: US 60/241, 573

; PRIOR FILING DATE: 2000-10-18

; PRIOR APPLICATION NUMBER: US 60/243, 643

; PRIOR FILING DATE: 2000-10-25

; PRIOR APPLICATION NUMBER: US 60/245, 256

; PRIOR FILING DATE: 2000-11-02

; PRIOR APPLICATION NUMBER: US 60/248, 395

; PRIOR FILING DATE: 2000-11-13

; PRIOR APPLICATION NUMBER: US 60/249, 826

; PRIOR FILING DATE: 2000-11-16

; PRIOR APPLICATION NUMBER: US 60/252, 303

; PRIOR FILING DATE: 2000-11-20

; PRIOR APPLICATION NUMBER: US 60/250, 981

; PRIOR FILING DATE: 2000-12-01

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: PERL Program

; SEQ ID NO 19

; LENGTH: 4888

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Incyte ID No. US20040029249A1 3533147CB1

US-10-399-645-19

Alignment Scores:

Pred. No.: 0 Length: 4888
Score: 3291.50 Matches: 624
Percent Similarity: 78.61% Conservative: 19
Best Local Similarity: 76.28% Mismatches: 63
Query Match: 62.86% Indels: 112
DB: 17 Gaps: 10

US-09-981-151D-8 (1-952) x US-10-399-645-19 (1-4888)

QY 211 AspPheCysPheTrpGlnGlySerLeuArgSerHisArgAsnSer----- 225
DB 285 GAATTCGCAATTATTGTGTGACATATAACGAATAGTTCACACAGCAATTATTCATTAA 344

QY 226 -----ProSerHisGlyGlyLysPheCys-GlyGlySerThrArgThrLeuLy 241
DB 345 TGTGGCCAAAGCAAATGCTCGTGGAATTTACAGAAAGTGACTTCAGGAGCTTCG 404
QY 241 sLeuCyAsnSerGlnLysCys-----ProArgAspSerVa 253
DB 405 T---GTTAACAGCCACCACTGCTGACCAAAAAAGGTCTAGAAATGCTCCTCAGGCCCT 461
QY 253 LAspPheArgAlaIaGlnCys-----AlaGlnHisAsnSerArgPheArgGlyAr 271
DB 462 GCAGTTCCACACTGTAACAATGTCTGGACTCATCCAGACAGCCCGCCCATGACGGGCT 521
QY 271 gHisTyrLysTrpLysProTyrThrGlnValGlnIaAspLeuCybLysLeuTyrCysIl 291
DB 522 TCACTAC-----GTGACATTAATTCAAGCATGATACG 554
QY 291 eaIaGlyLysPheAspPhePhe-----PheSerLeuSe 302
DB 555 AACAGAAAGAGGAGATTAATTCTTAAGGCCACTTCACACCTCTCATGGAAACTCGG 614
QY 302 rAsnLysValLysAspGlyThrProCysSer-----GluAspSerArgAsnValCy 319
DB 615 CAGAGCTGCCCAAGGCAAGCTCGCCATCCACGTACTGTACAAGACATCCACAGAGCCCA 674
QY 319 sIleAspGlyIleCybGluLeuSerValValSerThrSer-----AlaHis----- 334
DB 675 TGTCTCTGGGGCCAGTAGAGGTCTGTGTAACCTCAAGACATGGAGCTGGACATCAACC 734
QY 334 ----- 334
DB 735 CCTGCACAGCAGGCACTTCGGCTGGGACTGCCACAAAAGCAGCATTTCTGTGAAAGACG 794
QY 335 -----MetProGlnProProLySGluAspLeuPheIleLeuProAspGlyTyrLy 351
DB 795 CAAGAATAACATGCCCCCAGCCTCCCAAGGAAGACCTTTCATCTTGCCAGATGAGTATAA 854
QY 351 sSerCybLeuArgHisLysLysArgSerLeuLeuArgSerHisValArgAsnGlyGluLeuAsnVa 371
DB 855 GTCTTGCTTACGGCATTAAGCGCTCTCTTCTGAGGTCCCATAGAAAAGAAGAACTGAAACGT 914
QY 371 lGluThrLeuValValValAspLysLysMetMetGlnAsnHisGlyHisGluAsnIleTh 391
DB 915 GGAAGACCTTGGTGGTGTGACAAAAGATGATGCAAAACCATGGCCATGAAAATATCAC 974
QY 391 rThrTyrValLeuThrIleLeuAsnMetValSerAlaLeuPheLysAsp----- 407
DB 975 CACCTACGTGCTCAGATACTCAACATGGTATCTGCTTATTCAAGATGGAACAATAGG 1034
QY 407 ----- 407
DB 1035 AGGAAACATCAACATTGCAATTGTAGTCTGTATTCTTAGAAGATGAACAGCCAGGACT 1094
QY 408 -----GlyLe 409
DB 1095 GGTGATAAGTCACCAAGCAGACCAACCTTAAGTAGCTTCGCCAGTGGCAGTCTGATT 1154
QY 409 uMetGlyLysAspGlyThrArgHisAspHisAlaIleLeuLeuThrGlyLeuAspIleCy 429
DB 1155 GATGGGGAAGATGGGACTCGTCAAGCACGCGCATCTTACTGACTGCTGTGATATATG 1214
QY 429 sSerTrpLysAsnGluProCybAspThrLeuGlyPheAlaProIleSerGlyMetCysSe 449
DB 1215 TTCCTGGAAAGATGAGCCCTGTGCACTTTGGATTGGCAACCCATAAGTGAATGTGTAG 1274
QY 449 rLysTyrArgSerCysThrIleAsnGluAspThrGlyLeuGlyLeuAlaPheThrIleAl 469
DB 1275 TAAATATCGCAGCTGCACGATTAATGAAGATACAGGTCTTGACTGGCCTTCAACATTGC 1334
QY 469 ahIsGlySerGlyHisAsnPheGlyMetIleHisAspGlyGlyGlyAsnMetCysLysLy 489
DB 1335 CCATGAGTCTGACACAACAATTGGCATGATTCATGATGGAAGGAACAATGTGTAAAAA 1394
QY 489 sSerGlyGlyAsnIleMetSerProThrLeuAlaGlyArgAsnGlyValPheSerTrpSe 509

DB 1395 GTCCGAGGGGCAACATCATGTCTCCCTACATTGGCAGAGCAATGGAGTCTTCTCTGGTC 1454
QY 509 rProCysSerArgGlnTyrLeuHisLysPheLeuSerThrAlaGlnAlaIleCybLeuAl 529
DB 1455 ACCCTGACCGCCAGTATCTACACAATAATTTCTAAGCACCGCTCAAGCTATCTGCTTGC 1514
QY 529 aAspGlnProLysProValLysGlyTyrLysTyrProGlyLysLeuProGlyGlyLeuTy 549
DB 1515 TGATCAGCCAAAGCCTGTGAAGGAATACAAATTTCTGAGAAATTGCCAGAGAAATTATA 1574
QY 549 rAspAlaAsnThrGlnCysLysTrpGlnPheGlyGlyLysAlaLysLeuCybMetLeuAs 569
DB 1575 TGATGCAAACACACAGTGCAGAGTGGCAGTTGCCAGAGAAAGCCAAGCTTCGATGCTGGA 1634
QY 569 pPheLysLysAspIleCybLysAlaLeuTrpCysHisArgIleGlyArgLysCysGlyTh 589
DB 1635 CTTTAAAAAGGACATCTGTAAAGCCCTGTGTGCCATCGTAATTGGAAGAAATGTGAGAC 1694
QY 589 rLysPheMetProAlaIaGlyGlyThrIleCysGlyHisAspMetTrpCysArgGlyGly 609
DB 1695 TAAATTTATGCACAGCAGCAGAGGACAAATTTGTGGCATGACATGTGTGTCGGGAGG 1754
QY 609 yGlnCysValLysTyrGlyAspGlyGlyProLysProThrHisGlyHisTrpSerAspTr 629
DB 1755 ACAGTGTGTAATATGTGTATGAAGGCCCAAGCCACCCACCTAGCCACTGTGCGAAGT 1814
QY 629 pSerSerTrpSerProCysSerArgThrCysGlyGlyValSerHisArgSerArgLe 649
DB 1815 GTCTTCTGTGTCCTCCATGCTCAGAGACTGCGAGGGGAGTATCTCATAGAGTCCGCT 1874
QY 649 uCysThrAsnProLysProSerHisGlyGlyLysPheCysGlyGlySerThrArgThrLe 669
DB 1875 CTGCACCAACCCCAAGCCATGCATGAGGGAAGTTCTGTGAGGGCTCCACTCGCACTCT 1934
QY 669 uLysLeuCybAsnSerGlnLysCybProArgAspSerValAspPheArgAlaIaGlnCy 689
DB 1935 GAAGCTCTGCACAAGTCAAGAAATGTCCCGGGAAGTGTGTAACCTTCGTGCTCAAGTG 1994
QY 689 sAlaGlnHisAsnSerArgArgPheArgGlyArgHisTyrLysTrpLysProTyrThrGly 709
DB 1995 TGCCGAGCACACAAGACAGATTCAGAGGGCGGCACCTACAAGTGAAGCCTTACACTCA 2054
QY 709 nValGluAspGlnAspLeuCybLysLeuTyrCysIleAlaGlyLysPheAspPhePhePh 729
DB 2055 AGTAGAAGATCAGGACTTATGCAAACTCTACTGTATCGCAAGAGATTGATTCTTCTT 2114
QY 729 eSerLeuSerAsnLysValLysAspGlyThrProCysSerGlyAspSerArgAsnValCy 749
DB 2115 TTCTTTGTCAAATAAAGTCAAAAGATGGGACTCCATGCTCGGAGGATAGCCGTAATGTTTG 2174
QY 749 sIleAspGlyIleCybGlyLysValGlyCybAspAsnValLeuGlySerAspAlaValGly 769
DB 2175 TATAGATGGGATATGTGAGAGAGTTGGATGTGACAATGTCTTGGATCTGTGCTGTGA 2234
QY 769 uAspValCybGlyValCybAsnGlyAsnAsnSerAlaCysThrIleHisArgGlyLeuTy 789
DB 2235 AGACGTCTGTGGGGTGTGTAAACGGGAATACTCAGCCTGCACGATTCAACAGGGGTCTCTA 2294
QY 789 rThrLysHisHisHisThrAsnGlnTyrTyrHisMetValThrIleProSerGlyAlaAr 809
DB 2295 CACCAAGCACCAACACCAACCAAGTATTTACATGTGTCAACCATTCCTTGTGAGACCCG 2354
QY 809 gSerIleArgIleTyrGlyMetAsnValSerThrSerTyrIleSerValArgAsnAlaLe 829
DB 2355 GAGTATCCGCATCTATGAATGAACGTCCTTACCTCCTACATTTCTGTGCGCAATGCCCT 2414
QY 829 uArgArgTyrTyrLeuAsnGlyHisTrpThrValAspTrpProGlyArgTyrLysPheSe 849
DB 2415 CAGAAGTACTAAGTGAATGGGCACTGGACCGTGGACTGGCCCGGCGGTACAAATTTTTC 2474
QY 849 rGlyThrThrPheAspTyrArgArgSerTyrAsnGluProGluAsnLeuIleAlaThrGly 869

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Db      2475 GGGCACTACTTTGCACTACAGACGGTCTTAATAATGAGCCCGAGAACTTAATCGTACTGG 2534
QY      869 yPcrrThrAsngluThrLeuileValgluleuPheglnglyARgsnProglYValAl 889
Db      2535 ACCAACCAACGAGACACTGATATTGGAGCTGTGCTTTTCAGGGAAGAAACCGGGTGTTC 2594
QY      889 aTrpGluTyrsrMetProargLeuGlyThrGluLysglnProProAlaginProserTy 909
Db      2595 CTGGGAATACTCATGCTCTCGCTTGGGGACCGAGAAAGCAGCCCTGCCACGCTAGCTA 2654
QY      909 rThrTpAlaileValargSerGluCysserValserCysglYglYArg 926
Db      2655 CACTTGGGCATCGTGCCTCTGAGTGTCTCGTGTCTCTGCGAGGGGGAGCAG 2706

RESULT 13
US-10-363-937-34
; Sequence 34, Application US/10363937
; Publication No. US20040053269A1
; GENERAL INFORMATION:
; APPLICANT: Todd, Stephen; Delegeane, Angelo M.;
; APPLICANT: Gandhi, Ameena R.; Nguyen, Daniel B.;
; APPLICANT: Hafalia, April J.A.; Kearney, Liam;
; APPLICANT: Lu, Yan; Lee, Ernestine A.;
; APPLICANT: Chawla, Narinder K.; Das, Debopriya;
; APPLICANT: Arvizu, Chandra S.; Yao, Monique G.;
; APPLICANT: Kallick, Deborah A.; Elliott, Vicki S.;
; APPLICANT: Ding, Li; Yue, Henry;
; APPLICANT: Reddy, Roopa; Burford, Neil;
; APPLICANT: Baughn, Mariah R.; Lal, Preeti G.;
; APPLICANT: Borowsky, Mark L.; Lu, Dyung Ahn M.;
; APPLICANT: Ramkumar, Jayalaxmi; Yang, Junning;
; APPLICANT: Tribouley, Catherine M.; Khan, Farrah A.;
; APPLICANT: Gururajan, Rajagopal; Tang, Y. Tom;
; APPLICANT: Au-Young, Janice; Warren, Bridget A.;
; APPLICANT: Hernandez, Roberto; Duggan, Brendan M.
; TITLE OF INVENTION: PROTEASES
; FILE REFERENCE: PI-0212 USN
; CURRENT APPLICATION NUMBER: US/10/363, 937
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: PCT/US01/28161
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: US 60/231, 039
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US 60/232, 812
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/234, 850
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/236, 500
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 60/238, 773
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 60/239, 658
; PRIOR FILING DATE: 2000-10-11
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PERL Program
; SEQ ID NO 34
; LENGTH: 3389
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20040053269A1 7478405CB1
US-10-363-937-34

Alignment Scores:
Pred. No.:      7,12e-243      Length:      3389
Score:          2442.00      Matches:      486
Percent Similarity: 63.46%      Conservative: 127
Best Local Similarity: 50.31%      Mismatches:  208
Query Match:    46.64%      Indels:      147
DB:             18      Gaps:          22

US-09-981-151D-8 (1-952) x US-10-363-937-34 (1-3389)

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QY	46	ProArgLeuLeuSerArgGlyProArgArgLeuThrAlaMetSerProLeuPheSerAla	65	
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DB	42	CCGGCTTGCCACCCGACGCCGGCGTCCGCACCTGACCA	92	
		-----	-TGAATGCC	
QY	66	GlyThrCys-----	-ValArgHisGlyThr--Arg	74
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DB	93	CCCTCTGCTCGCGTGCCTTCCCGGCTCGGGGTTCCGGCCCCCGACGGGCTGCGCG	152	
QY	75	SerGlySerAlaTrp-----	-----GluPro	81
DB	153	GACTGGGGCGCGTGGCCCAAGCGCTCCAGCTGTGCTCCCTCTGCTGTGCGTCCGTCGCCG	212	
QY	82	GluArgProAlaSerSerSerThrArgGlyAlaAlaGlyLeuAspGlyLysGlyArgAsp	101	
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DB	213	CGGCGCTTA-GCCAGTGACAGCAGCAGCGCGCCAGCGGATTAAT	256	
QY	102	MetAspGluAlaGlyAsnHisArgSerGlnGlnThrAsnThrGlyThrGluAsnGlnThr	121	
DB	256	-----	-----	256
QY	122	LeuHisValLeuThrGlnTyrAspLeuValSerAlaTyrGluValAspHisArgGlyAsp	141	
DB	257	-----GATGATTACGTCCTTGTGCACGCCAGTAGAAGTACACGCCGGGTCA	304	
QY	142	TyrValSerHisGluIleMetHisHisGlnArgArgArgAlaValAlaValSerGln	161	
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DB	305	TATATTTCACAGCAGCATTTTGCACACAGCAGCAAAAGCATCG--GCGCAGAATGCC	361	
QY	162	ValGluSerLeuHisLeuArgLeuLysGlyProArgHisAspPheHisMetAspLeuArg	181	
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DB	362	AGAACTCCCTGCACCTACCGATTTCAGCATTTGACAGAACTGCACCTTAGAAGTTAAG	421	
QY	182	ThrSerSerSerLeuValAlaProGlyPheIleValGlnThrLeuGlyLysThrGlyThr	201	
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DB	422	---CCCTCGGCAATTTTGAGCAGTCACCTTATGTGCCAGGTACTTGAAAAGATGTGCT	478	
QY	202	LysSerValGlnThrLeuProProGluAspPheCysPheTyrGlnGlySerLeuArgSer	221	
DB	479	TCAGAGACTCAGAAA--CCCGAGGTGCAGCAATGCTTCTATCAGGAGTTTATCAGAAAT	535	
QY	222	HisArgAsnSerProSerHisGlyGlyLysPheCysGluGlySerThrArgThrLeuLys	241	
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DB	536	GAC--AGCTCTCTCTGTGTGCTGTGTCTACGTCGTGCTGCTTGCAGGTTTAATAGG	592	
QY	242	LeuCysAsnSerGln-----LysCysProArgAspSerValAspPheArgAla	257	
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DB	593	ACACGAAAAAATGAATTCCTCATCTCGCATTTACCTCAG-----	631	
QY	258	AlaGlnCysAlaGlnHisAsnSerArgArgPheArgGlyArgHisIleTyrLysTrpLysPro	277	
DB	632	CTTCTGGCCAGAAACACAACACTACGCTCCCTGGCGGTCAACAT-----CCT	679	
QY	278	TyrThrGlnValGluAlaAspLeuCysLysLeuTyrCysIleAlaGlnGlyPheAsp--	296	
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DB	680	CACGTACT-GTACAAAAGAC-----AGCAGAGGAAGATCSA	717	
QY	297	-----PhePhePheSerLeuSerAsnLysVal--LysAspGly	308	
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DB	718	GCGGTACCGTGECTACCCCGGCTCTGCGCGGAATTAATCTGTACTCCCAAGTCACAT	777	
QY	309	ThrProCysSerGluAspSerArgAsn--ValCysIleAspGlyIleCysGluLeuSer	327	
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DB	778	TCCCCATGATCTCAGAGTGCAGAGACAGATTCACCATCGAAGGTTGCAAAAGCAGCA	837	
QY	328	ValVal---SerThr-SerAlaHisMetProGlnProProLysGluAspLeuPheIleLe	346	
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DB	838	TTTTTGTGACGACGCAAGAAATATGCTCCCAAGCTCCACAGAGACACCTATCTAAG	897	
QY	346	uProAspGlyTyrLysSerCysLeuArgHisLysValArgSerLeuLeuArgSerHisArgAs	366	
DB	898	GTTTGATGAATATGGAGCTCTGGCGGACCCAGAGATCAGCTGGAATAATCACAAGAGG	957	

QY	366	nglglululeuasnvalgluthrileuvalvalasplyslysmetmetglasnhsigl	386
Db	958	C-----CTCATGTGGAAACCCCTCGTGGTGGCAGACAAGAAAAATGGTGAANAACATGG	1011
QY	386	yhisgluasnilethrthryrvalleuthrileleuasnmetvalseralaleuphely	406
Db	1012	CAAGGAAATGTCACACATACATTCTCACAGTAATGAACATGTTTCTGGCCTATTAA	1071
QY	406	saasply-----	408
Db	1072	AGATGGGACTATTGGAAGTGACATAACGTGTTGTGGTGAGCCTAATTCTTGGAAACA	1131
QY	408	-----	408
Db	1132	AGAACCTGAGGATTATTGATCAACCATCATGACAGCACCAAGTCCTGAATAGTTTTGTCA	1191
QY	409	-----leumetglylysaasplythrarghisasphisalaleuleuth	424
Db	1192	ATGGCAGTGTGCCCCCTCATTTGGAAAGAATGGCAGAGACATGATCCATCTTAATAAC	1251
QY	424	rglyleuasplylecyseretrplysasngluprocysaspthrleuglyphealaproi	444
Db	1252	AGGATTTGATATTGTTCTTGGAAGAATGAACCATGTGACACTTAGGGTTGGCCCCCAT	1311
QY	444	eSerglymetcysserlystyrargsercysthrileasngluaspthrlyleuglyle	464
Db	1312	CAGTGAATGTGCTCTAAGTACCGAAGTTGTACCATCAATGAGSACACAGACTTGCCCT	1371
QY	464	uAlaphethrilealahnisgluserglyhisasnphelymetilehisasplyglul	484
Db	1372	TGCCTTCACCATCGCTCATGAGTCAGGGCACAACTTTGGTATGATTCCAGCGSAGAAAG	1431
QY	484	yasnmetcyslysllysserglulyasnilemetserprothrleualaglyargasn	504
Db	1432	GAATCCCTGCAGAAAGCGTGAAGGCATATCATGTCTCCACACTGACCGGAAACAATGG	1491
QY	504	yAlpheSertrpserProCysSerArgglntyrleuhslysbphelusethralagl	524
Db	1492	AGTGTTCATGTGCTCTCTCGACGCCAGCATATCTCAGAAATTCCTCAGACACCTCA	1551
QY	524	nalalilecysleualaaspglnpPolysProvallybglutyrlstyrProglulysle	544
Db	1552	GCGCGGGGTGTCTAGTGATGAGCCCAAGCAGACGACATTAATATCCGACAAACT	1611
QY	544	uProglyluleutyrrasparaasnThrglncyslysttrpglnphelyglulysalaly	564
Db	1612	ACCAGACAGATTTATGATGCTGACACACAGTGTAAATGGCAATTTGGAGCAAAAGCCAA	1671
QY	564	sleuCyasmetleuasbpPhelyslysaaspilecyslysalaleuTrpCysHisargile	584
Db	1672	GTTATGACAGCCTTGCTTTGTGTAAGGATATTGCAAAATCACATTGTTGGTCCAGAGTAGG	1731
QY	584	yArglysCyegluthrlyasphemetProalalaglulythrileCysglyhisaspm	604
Db	1732	CCACAGGTGTGAGAACCAAGTTTATGCCCGCAGCAGAAAGGACCGTTGTGCTTGAGTAT	1791
QY	604	tTrpCyasargglyglincysvallystyrglyaspgluglypPolysProThrhsgl	624
Db	1792	GTTGTGTGGCAAGGCCAGTGTCTAAAGTTGGGGAGCTCGGGCCCCGCCATCCACGG	1851
QY	624	yHisTrpSeraspTrpserSerTrpserProCysSerArgthrCysglyglyvalse	644
Db	1852	CCAGTGTTCGCGCTGTGTCGAAGTGTCAGAATGTTCGCCGACATGTGGTGAAGAGTCAA	1911
QY	644	rHisargSerargleuCysthraaspProlysProserHisglglylyspheCysglul	664
Db	1912	GTTCCAGGAGACACTGCATTAACCCCAAGCCTCAGTATGTGGCATATATCTGTCCAGG	1971
QY	664	ySerThrArgthrleuylsleuCyasnserserGlnlysCysProargaspSerValasph	684
Db	1972	TTCTAGCCGATTTATCAGCTGTGCATATATTAACCTTGCAATGAANAATAGCTTGATTT	2031
QY	684	eArgalalaglnCysalaglunhisasnserArgargpheararglylArgHisTyrlystr	704

Db	2032	TCGGGCTCAACAGTGTGCAGATATATAACGCAAACTTTCCGTGATGTTCTACCAAGTG	2091
QY	704	PLYSProTYrThrGlnValGluAspGlnAspLeuCybLysLeuTYrCysIleAlaGluG1	724
Db	2092	GAACCCCTATACAAAAGTGGAAGAGAAGATCGATGCAAACTGACTGCAAGCTGAGAA	2151
QY	724	YPheAspPhePhePheSerLeuSerAsnLysValLysAspGlyThrProCysSerGluAs	744
Db	2152	CTTTGAATTTTTTTTGGCAATGTCCGGCAAAAGTGAAAGATGGAACCTCCGTCCCAAA	2211
QY	744	pSerArgAsnValCysIleAspGlyIleCysGluArgValGlyCysAspAsnValLeuG1	764
Db	2212	CAAAAATGATGTTTGTATGTACGCGGTTTGTGAACCTAGTGGAGATGTGATCATGAAC	2271
QY	764	YSerAspAlaValGluAspValCysGlyValCysAsnGlyAsnAsnSerAlaCysThrI1	784
Db	2272	CTCTAAAGCAGTTTCAGATGCTTGTGGCGCTTGGCAAGGTGATTAATTCACCTTGCAAG	2331
QY	784	eHisArgGlyLeuTYrThrLysHisHisIsthAsnGlnTYrTYrHisMetValThrI1	804
Db	2332	TTATAAAGCCTGTACTCAACACGACATPAAAGCAAAATGATATTATCCGGTGTATCAT	2391
QY	804	eProSerGlyAlaArgSerIleArgIleTYrGluMetAsnValSerThrSerTYrIleSe	824
Db	2392	TCCAGCTGGCGCCCGAAGCATCGAAATCCAGAGCTGCAGGTTTCCCTCCAGTTACCTCG	2451
QY	824	rValArgAsnAlaLeuArgArgTYrTYrLeuAsnGlyHisIsthProThrValAspTrpProG1	844
Db	2452	AGTTCAAGCCTCAGTCAAAAGTATTACTTCAACGGGGCTGAGCATGACATGGCTGG	2511
QY	844	YArgTYrLysPheSerGlyThrThrPheAspTYrArgArgSerTYrAsnGluProGluAs	864
Db	2512	GGAGTTCCTCCCTTGCCTGGGACCAACGTTGAATACCAAGCGCTTTCAACCGCCCGAAACG	2571
QY	864	nLeuIleAlaThrGlyProThrAsnGluThrLeuIleValGluLeuLeuPheGlnGlyAr	884
Db	2572	TCTGTACGGCCACGAGGCCCAAAATGAGACGCTGTCTTGAATTCGTATGCAAGGCAA	2631
QY	884	gAsnProGlyValAlaTrpGluTYrSerMetProArgLeu-----GlyThrGluLysG1	902
Db	2632	AAATCCAGGGATAGCTTGAAGATGACACTTCCCAAGCTCATGATGAACT-----	2683
QY	902	nProProAla-----GlnProSerTYrThrTrpAlaIleValArgSerGluCysSerVa	920
Db	2684	-CCACCAAGCCACAAAAGACCTGCCTATATCTGAGATTCGTGACAGTCAAGTGTCCGT	2742
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; Sequence 1, Application US/10240545A			
; Publication No. US20030185828A1			
; GENERAL INFORMATION:			
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.			
; TITLE OF INVENTION: No. US20030185828A1el aggreganase			
; FILE REFERENCE: 08959.0002			
; CURRENT APPLICATION NUMBER: US/10/240,545A			
; CURRENT FILING DATE: 2002-10-02			
; PRIOR APPLICATION NUMBER: PCT/JP01/11033			
; PRIOR FILING DATE: 2001-12-17			
; PRIOR APPLICATION NUMBER: JP 2000-384300			
; PRIOR FILING DATE: 2000-12-18			
; NUMBER OF SEQ ID NOS: 26			
; SEQ ID NO 1			
; LENGTH: 3666			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (1)..(3666)			


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Db      1785  GTCGAAGTGTGCAGAATGTTCCCGGACATGTGTGAGAGAGTCAAGTTCAGAGAGACA 1844
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Db      1845  CTGCAATTAACCCCAAGCCTCAGTATGTGTGCTTATCTGTCCAGGTTCTAGCCGATTTA 1904
Qy      669  uLysLeuCysAsnSerGlnLysCysProArgAspSerValAspPheArgAlaIaGlnCy 689
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Db      1905  TCAGCTGTGCAATATTAAACCTTGCAATGAAAATAGCTTGATTTTCGGGCTCAACAGTG 1964
Qy      689  sAlaGlnHisAsnSerArgArgPheArgGlyArgHisTyrLysTyrLysProTyrThrGl 709
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Db      1965  TGCAGATATATAACAGCAAACTTTCGCTGATGGTTCTACAGTGGAAAACCTATACAAA 2024
Qy      709  nValGluAspGlnAspLeuCysLysLeuTyrCysIleAlaGluGlyPheAspPhePhe 729
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Qy      729  eSerLeuSerAsnLysValLysAspGlyThrProCysSerGlnAspSerArgAsnValCy 749
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Db      2085  TGCATATGTCGGCAAGTGAAGAAGTGAAGTCCCTGCTCCCAACAAAATGATGTTTG 2144
Qy      749  sIleAspGlyIleCysGluArgValGlyCysAspAsnValLeuGlySerAspAlaValGl 769
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Db      2145  TATTGACGGGGTTGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTTC 2204
Qy      769  uAspValCysGlyValCysAsnGlyAsnAsnSerAlaCysThrIleHisArgGlyLeuTy 789
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Db      2205  AGATGCTGTGCGCTTTCGCAAGGTGATTAATTCACCTTGCAAGTTTATTAAGCCTGTA 2264
Qy      789  rThrLysHisHisHisThrAsnGlnTyrTyrHisMetValThrIleProSerGlyAlaAr 809
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Qy      809  gSerIleArgIleTyrGluMetAsnValSerThrSerTyrIleSerValArgAsnAlaLe 829
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Db      2325  AACGATCGAAATCCAGGAGCTGCAGCTTCTCCAGTTAACCCTCGAGTTGGAAGCCTCAG 2384
Qy      829  uArgArgTyrTyrLeuAsnGlyHisTyrThrValAspTyrProGlyArgTyrLysPheSe 849
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Db      2385  TCAAAAGTATTACTCTACCGGGGCTGAGACATCGACTGGCTGGGGAGTTCCCTTCGC 2444
Qy      849  rGlyThrThrPheAspTyrArgArgSerTyrAsnGluProGluAsnLeuIleAlaThrGl 869
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Db      2445  TGGGACCAACGTTGAATACCAAGCGCTCTTTCACACCGCCCGGAACGCTGTACGCCCA 2504
Qy      869  yProThrAsnGluThrLeuIleValGluLeuPheGlnGlyArgAsnProGlyValAl 889
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Db      2505  GCCCACAAAATGAGACGCTGCTTGAATTCGTGATGCAAGGCAGAAAATCCAGGATAGC 2564
Qy      889  aTyrGluTyrSerMetProArgLeu-----GlyThrGluLysGlnProProAla----- 905
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Qy      906  -GlnProSerTyrThrTyrPalaIleValArgSerGluCysSerValSerCysGlyGlyGl 925
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Qy      925  y 925
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; PRIOR APPLICATION NUMBER: 60/353,680
; PRIOR FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3219
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-354-983-3

Alignment Scores:
Pred. No.:      1,07e-242      Length:      3219
Score:          2440.00        Matches:      471
Percent Similarity: 65.89%      Conservative: 124
Best Local Similarity: 52.16%      Mismatches:  190
Query Match:    46.60%          Indels:       119
DB:             18             Gaps:       18

US-09-981-151D-8 (1-952) x US-10-354-983-3 (1-3219)
Qy      85  AlaSerSerSerThrArgGlyAlaAlaGlyLeuAspGlyLysGlyArgAspMetAspGlu 104
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      70  GCCAGTGACAGCAGCAGCGCGCCAGCGGATTAAT----- 105
Qy      105  AlaGlyAsnHisArgSerGlnGlnThrAsnThrGlyThrGluAsnGlnThrLeuHisVal 124
        -----
Db      105  ----- 105
Qy      125  LeuThrGlnTyrAspLeuValSerAlaTyrGluValAspHisArgGlyAspTyrValSer 144
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      106  ---GATGATTACGCTTTGTGACCGCCAGTAGAAGTAGACTGACCGCGGTCAATATTTC 162
Qy      145  HisGluIleMetHisHisGlnArgArgArgAlaValAlaValSerGluValGluSer 164
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      163  CACGACATTTGCAACAACGGCAGGAAAAAGCGATCG--GCCAGAATGCCAGAAAGCTCC 219
Qy      165  LeuHisLeuArgLeuLysGlyProArgHisAspPheHisMetAspLeuArgThrSerSer 184
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      220  CTGCACTACCGATTTTCAGCATTTTGACAGAGAACTGCACCTTAGAACTTAAG---CCCTCG 276
Qy      185  SerLeuValAlaProGlyPheIleValGlnThrLeuGlyLysThrGlyThrLysSerVal 204
        ::||| ::||| ||||| ||||| ||||| ||||| ||||| |||||
Db      277  GCGATTTTGAGCAGTCACCTTAATTGTCCAGGTACTTGAAAAGATGGTGCTTCAGAGACT 336
Qy      205  GlnThrLeuProProGluAspPheCysPheTyrGlnGlySerLeuArgSerHisArgAsn 224
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      337  CAGAAA--CCGAGGTGCAGCAATGCTTTATCAAGGATTTATCAGAAATGAC--AGC 390
Qy      225  SerProSerHisGlyGlyLysPheCysGluGlySerThrArgThrLeuLysLeuCysAsn 244
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      391  TCCTCCTGTGCGCTGTGTCTACGTGTGCTGCTGTGTACAGGTTTAATAAGGACACGAAAA 450
Qy      245  SerGln-----LysCysProArgAspSerValAspPheArgAlaIaGlnCys 260
        ::||| ::||| ||||| ||||| ||||| ||||| ||||| |||||
Db      451  AATGAATTCCTCATCTCGCAATTACCTCAG-----CTTCTGGCC 489
Qy      261  AlaGlnHisAsnSerArgArgPheArgGlyArgHisTyrLysTyrLysProTyrThrGln 280
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      490  CAGGAACACAAACACAGCTCCCTGCGGTCACCAT-----CCTCACGTACT- 536
Qy      281  ValGluAlaAspLeuCysLysLeuTyrCysIleAlaGluGlyPheAsp----- 296
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      537  GTACAAAAGGAC-----AGCAGAGGAGAAAGATCCAGCGGTACCG 575
Qy      297  -----PhePhePheSerLeuSerAsnLysVal---LysAspGlyThrProCys 311
        ::||| ::||| ||||| ||||| ||||| ||||| ||||| |||||
Db      576  TGGCTACCCCGGCTGTGCGGGAATTATCTGTACTCCCAAGTCAACATTCGCCATGCG 635
Qy      312  SerGluAspSerArgAsn---ValCysIleAspGlyIleCysGluLeuSerValVal--- 329
        ::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      636  ATCTCAGAGTGAAGACAGACAGATATCACCATCGAAAGGTTGCAAAAAGCAGCATTTTGTGG 695
Qy      330  SerThr-SerAlaHisMetProGlnProProLysGluAspLeuPheIleLeuProAspGl 349
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Db 696 ACGACGCAAGAAATATGCTCCCAAGCCTCCACAGAGACACCTATCTAAGTTTGATGA 755
QY 349 uTyrLysSerCyLeuArgH1blybArgSerLeuArgSerH1sArgbAngluLe 369
Db 756 ATATGGAGCTCTGGCGGACCCCAAGATCAGCTGGAAAATCACAAGAGGC-----CT 809
QY 369 uAsnValGluThrLeuValValAspLysbMetMetGlnAsnH1sGlyH1sGluAs 389
Db 810 CAATGTGGAACCTCGTGTGGGACAGACAAGAAAATGGTGAAAAGCATGGCAAGGAAA 869
QY 389 nIleThrThrTyrValLeuThrIleLeuAsnMetValSerAlaLeuPheLysArgLy-- 408
Db 870 TGTCAACCATACATCTCTCACAGTAATGAACATGTTTCTGGCCTATTTAAGATGGGAC 929
QY 408 ----- 408
Db 930 TATTGGAAGTACATAAACGTGGTTGTGTAGCCTAATTCTTGGACACAGAACCCTGG 989
QY 408 ----- 408
Db 990 AGGATTATTGATCAACCATCATGACAGACCAAGTCTGTGAATAGTTTGTCAATGGCAGTC 1049
QY 409 ----LeuMetGlyLysAspGlyThrArgH1sAspH1sAlaIleLeuLeuThrGlyLeuAs 427
Db 1050 TGCCCTCATTTGGAAGAATGGGCAAGACATGATCCATCTTAACACAGATTGGA 1109
QY 427 nIleCySerSerTrpLysAsnGluProCyAspThrLeuGlyPheAlaProIleSerGlyMe 447
Db 1110 TATTTGTTCTTGGAGAAGATGAACCATGTGACACTCTAGGGTTTGGCCCCCATCATGGAAAT 1169
QY 447 tCySerSerLysTyrArgSerCySerThrIleAsnGluAspThrGlyLeuGlyLeuAlaPheTh 467
Db 1170 GTGCTCTAAGTACCGAAGTGTATCATCAATGAGSACACAGGACTTGGCCTTGCTTCAC 1229
QY 467 rIleAlaH1sGlySerGlyH1sAsnPheGlyMetIleH1sAspGlyGlyLeuAsnMetCy 487
Db 1230 CATCGCTCATAGTCAAGGACAACTTTGGTATGATTCAACGACGAGAAAGGAAATCCCTG 1289
QY 487 sLysLysSerGlyGlyAsnIleMetSerProThrLeuAlaGlyArgbAnglyValPheSe 507
Db 1290 CAGAAAGGCTGAAGGCAATATATGTCTCCACACTGACCCGGAACAATGGAGTGTTC 1349
QY 507 rTrpSerProCySerArgGlnTyrLeuH1blybPheLeuSerThrAlaGlnAlaIleCy 527
Db 1350 ATGGTCTTCTTGCAAGCCGCCAGTATCTCAAGAAATTCCTCAGACACACCTCAGCGGGGTG 1409
QY 527 sLeuAlaAspGlnProLysProValLysGlyTyrLysTyrProGluLysLeuProGlyG1 547
Db 1410 TCTAGTGGATGAGCCCAAGCAAGCAGACAGATATAATATCCGGAACAACCTACAGGACA 1469
QY 547 uLeuTyrAspAlaAsnThrGlnCyLysTyrGlnPheGlyGluLysAlaLysLeuCyAsMe 567
Db 1470 GATTATGATGCTGACACACAGTGTAAATGGCAATTGGAGCAAAAGCCAAAGTTATGCAAG 1529
QY 567 tLeuAspPheLysLysAspIleCyLysAlaLeuTrpCyH1sArgIleGlyArgLysCy 587
Db 1530 CTTGGTTTGTGAAGGATATTGGCAATCACTTTGGTGCCACCGAGTAGGCCACAGGTG 1589
QY 587 sGluThrLysPheMetProAlaAlaGlyGlyThrIleCySgIyH1sAspMetTrpCyAsr 607
Db 1590 TGAACCAAGTTTATGCCCGGACAGAGGGAACCGTTGTGGCTTGAGTATGTGTGTG 1649
QY 607 gGlyGlyGlnCyValLysTyrGlyAspGlyGlyProLysProThrH1sGlyH1sTrpSe 627
Db 1650 GCAAGGCCAGTGCATAAGTTGGGGAGCTGGGGCCCGGCCCATCCAGGCCAGTGTGTC 1709
QY 627 rAspTrpSerSerTrpSerProCySerArgThrCySgIyGlyGlyValSerH1sArgSe 647
Db 1710 CGCCTGTGGAAGTGTCAGAATGTCCCGGACATGTGTGAGGAGTCAAGTTCACAGA 1769
QY 647 rArgLeuCyThrAsnProLysProSerH1sGlyGlyLysPheCySgIySerThrAr 667

Db 1770 GAGACATGCAATAACCCCAAGCCTCAGTATGGTGCAATTTCTGTCCAGGTTCTAGCCG 1829
QY 667 gThrLeuLysLeuCyAsnSerGlnLysCybProArgAspSerValAspPheArgAlaI 687
Db 1830 TATTATGACCTGTGCATATTTAAACCTTGCATATGAATAATAGCTTGATTTTCGGGCCCA 1889
QY 687 aGlnCySgIaGluH1sAsnSerArgArgPheArgGlyArgH1sTyrLysTrpLysProTy 707
Db 1890 ACAGTGTGAGAATATATACAGCAAAACCTTCCGTGATGGTTCTTACCAAGTGGAACCCCTA 1949
QY 707 rThrGlnValGluAspGlnAspLeuCybLysLeuTyrCySgIleAlaGlyGlyPheAspPh 727
Db 1950 TACAAAAGTGAAGAGAGATGATGACAAACTGTACTGCAAGGCTGAGAACTTTGAATT 2009
QY 727 ePhePheSerLeuSerAsnLysValLysAspGlyThrProCySerGluAspSerArgAs 747
Db 2010 TTTTTCATGATGTCCGGCAAGTGAAGATGGAACCTCCTGCCCAACAGAAATGA 2069
QY 747 nValCySgIleAspGlyIleCySgIuArgValGlyCyAspAsnValLeuGlySerAspAl 767
Db 2070 TGTTTGATTTGACGGGGTTGTGAACTAGAGTGGATGTATCAATGAACCTCTAAAGC 2129
QY 767 aValGluAspValCySgIyValCyAsnGlyAsnAsnSerAlaCySthrIleH1sArgG1 787
Db 2130 AGTTTCAGATGCTGTGGCGTTTGCAAGGTGATTAATCAACTTGCAAGTTTATAAAG 2189
QY 787 yLeuTyrThrLysH1sH1sH1sThrAsnGlnTyrTyrH1sMetValThrIleProSerG1 807
Db 2190 CCTGTACTCAACSCAGCATAAAGCAATGAATATATTCCGGTGTATCATTCACAGCTGG 2249
QY 807 yAlaArgSerIleArgIleTyrGluMetAsnValSerThrSerTyrIleSerValArgAs 827
Db 2250 CGCCGGAAGCATGAAATCCAGAGCTGCAGGTTTCTCCAGTTACCTGCAGTTCGAAG 2309
QY 827 nAlaLeuArgArgTyrTyrLeuAsnGlyH1sTrpThrValAspTrpProGlyArgTyrLy 847
Db 2310 CCTCAGTCAAAAGTATTAACCTCACCGGGGGCTGAGCATGCACTGGCGTGGAGATTCCC 2369
QY 847 sPheSerGlyThrThrPheAspTyrArgArgSerTyrAsnGluProGluAsnLeuIleAl 867
Db 2370 CTTCGTGGGACCAAGTGTGAATACAGCGCTCTTCAACCGCCGGAACGTCTGTACGC 2429
QY 867 aThrGlyProThrAsnGluThrLeuIleValGlyLeuLeuPheGlnGlyArgAsnProG1 887
Db 2430 GCCAGGGCCCAAAATGAGACGCTGGTCTTTGAATCTGATGCAAGGCAAAAATCCAGG 2489
QY 887 yValAlaTrpGluTyrSerMetProArgLeu-----GlyThrGluLysGlnProProAl 905
Db 2490 GATAGCTTGGAAAGTATGCACTCCCAAGTCAATGAATGAACT-----CCACCAAGC 2540
QY 905 a-----GlnProSerTyrThrTrpAlaIleValArgSerGluCySerValSerCyG1 923
Db 2541 CACAAAAGACCTGCCATATACCTGAGTATCGTGCAGTCAAGTGTCTCGTCTGTGG 2600
QY 923 yGlyGly 925
Db 2601 TGAAGGT 2607

Search completed: September 10, 2005, 03:04:41
Job time : 1388 secs